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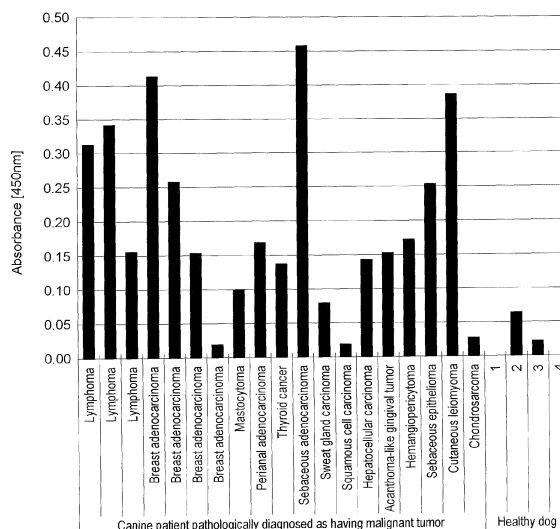
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(54) **Cancer detection method**

(57) The present invention relates to a method for detecting cancer, comprising measuring the expression of a polypeptide having a reactivity of binding to an antibody against a CAPRIN-1 protein having an amino acid sequence shown in any one of the even-numbered SEQ ID NOS: 2-30 in the Sequence Listing via an antigen-

antibody reaction in a sample separated from a living organism, and, a reagent for detecting a cancer comprising the CAPRIN-1 protein or a fragment thereof, an antibody against the CAPRIN-1 protein or a fragment thereof, or a polynucleotide encoding the CAPRIN-1 protein or a fragment thereof.

Fig. 3



Description

TECHNICAL FIELD

5 **[0001]** The present invention relates to a method for detecting cancer using CAPRIN-1 as a tumor marker.

BACKGROUND ART

10 **[0002]** Cancer is the leading cause of death. Treatment currently performed for cancer is mainly symptomatic therapy that mostly consists of surgical therapy with a combination of radiation therapy and chemotherapy. Owing to advancements in medical technology, cancer is now almost a curable disease if it can be detected early. Hence, a method for detecting cancer, by which detection can be conveniently performed using serum, urine, or the like without imposing physical or economic burdens on cancer patients, is now required.

15 **[0003]** As a cancer diagnostic method using blood or urine, a method for measuring a tumor product such as a tumor marker has recently become popular. The term "tumor product" refers to a tumor-associated antigen, an enzyme, a specific protein, a metabolite, a tumor gene, a tumor gene product, a tumor suppressor gene, and the like. Carcinoembryonic antigen CEA, glycoprotein CA19-9, CA125, prostate-specific antigen PSA, calcitonin, which are peptide hormones produced in the thyroid and the like are used as tumor markers for diagnosis of some cancer types. However, tumor markers useful for cancer diagnosis are absent for many cancer types. Also, most currently known tumor markers
20 are present in only trace amounts (on roughly a pg/mL order) in body fluids. Therefore, highly sensitive measurement methods or special techniques are required for detecting such tumor markers. Under the current circumstances, it is expected that provision of a new cancer testing means capable of detecting various types of cancer with high sensitivity involving a convenient procedure creates diagnostic applications for various types of cancer.

25 **[0004]** Also, such cancer testing means is very useful if it is capable of not only detecting cancer but also diagnosing cancer having developed in a location invisible to the naked eye, the extent of cancer, the malignancy or postoperative course of cancer, recurrence, metastasis, and the like.

[0005] Specifically, if diagnosis of cancer that has developed in a location invisible to the naked eye becomes possible, such cancer testing means would be useful for early detection of cancer within a location such as an intraperitoneal part that is difficult to recognize. Also, a tumor that does not have a grossly visible size such as cancer that is undetectable
30 even by ultrasonography, CT (computer tomography), or MRI (nuclear magnetic resonance imaging) can be detected.

[0006] Additionally, the extent of cancer is classified based on the degree to which a tumor spreads at the primary site and the presence or the absence of metastasis to regional lymph nodes or distant organs. In general, there are 5 disease stages (each referred to as "stage"), and higher stage numbers indicate more advanced stages of the disease. Strictly, the definition of stage differs depends on organs. However, for example, cancer at stage 0 is cancer that remains
35 intraepithelial and cancer at stage IV is cancer that has metastasized to a distant location. If such extent of cancer is found, decisions about appropriate treatment courses as well as diagnosis of the therapeutic effects of an anticancer agent become possible. As specific examples of decisions about treatment courses, in the case of prostate cancer and the like, there is a type requiring no treatment because it has very low malignancy and will almost never progress. In contrast, there is a type requiring treatment because it is progressive and metastasizes to bone or the like and causes
40 patients to die painfully. Therapies such as hormone therapy and extirpative surgery are each associated with an adverse reaction. Thus, therapies should be appropriately determined and decided upon. Also, if evaluation concerning the selection of an anticancer agent can be appropriately made or if timing or the like for the termination of administration of an anticancer agent can be appropriately determined, physical and economical burdens on patients can also be reduced. Therefore, it is important to be able to diagnose the extent of cancer.

45 **[0007]** One of the characteristics of cancer cells is that they undergo blastogenesis; that is, dedifferentiation. Except for some cancer types, poorly differentiated or undifferentiated cancer cells with a low degree of differentiation rapidly grow after metastasis and result in poor prognosis after therapy. Such cancer is said to have high malignancy. Conversely, highly differentiated cancer cells with a high degree of differentiation retain the structural and functional characteristics of affected organs. Such cancer can be said to have relatively low malignancy. If the malignancy of cancer can be
50 determined, the following measures can be taken. Even if the tumor is small, a wide surgical margin can be secured upon tumor removal, when the malignancy is high. Moreover, follow-up is possible while paying attention to a wide range of peripheral tissue.

[0008] If diagnosis of postoperative courses including recurrence and metastasis is possible, diagnosis of whether or not a tumor can be completely removed by surgery becomes possible. Incomplete tumor removal likely results in recur-
55 rence. Hence, such diagnosis can provide criteria for determining to more carefully perform follow-up at short intervals or to perform early reoperation if necessary. Also, if recurrence takes place, there is a high possibility of early detection. Detection is often delayed when distant metastasis takes place. However, if diagnosis of metastasis becomes possible, it becomes possible to provide criteria by which the range of testing can be broadened to include areas other than the

site of removal and the periphery thereof.

[0009] It is known that dogs grow old 7 times faster than humans. Recently, companion animals are being raised as family members and often have lifestyle habits similar to those of their owners. Therefore, it is predictable that an owner's risk of developing cancer would be high when his or her companion animal develops cancer. If convenient and precise cancer diagnosis becomes possible for companion animals, it would be expected to provide clues for preventing cancer of owners.

[0010] Currently, the number of domestic dogs in Japan is said to be about 6,700,000, and the same figure for the U.S. is said to be about 17,640,000. Quintuple, septuple, and octuple combined vaccines and the like have become prevalent, in addition to rabies shots, and thereby highly lethal infectious diseases have decreased, such as canine parvovirus infection, canine distemper virus infection, canine parainfluenza (kennel cough), canine adenovirus-2 infection (kennel cough), infectious canine hepatitis, canine coronavirus infection, and leptospirosis. Therefore, the average life span of dogs has increased. Elderly dogs, which are seven years old or older, account for 35.5% of all domestic dogs. Causes of death of domestic dogs are also similar to those of humans, such as cancer, hypertension, and cardiac disease, which are on the rise. In the U.S., about 4,000,000 dogs are diagnosed with cancer annually. Also in Japan, it is said that about 1,600,000 dogs are potentially affected with tumors.

[0011] However, convenient cancer diagnostic agents for animals have been absent. Furthermore, in animal medical care, testing methods that involve photographing or filming using X-rays, CT scans, MRI scans, or the like have not been prevalent. After palpation, a simple blood test, and testing using X-ray photography are performed, diagnosis currently depends significantly on the experience of veterinarians. Testing methods using serum have been partially begun, but the methods use human tumor markers since no canine tumor marker has been discovered.

[0012] Precise cancer diagnosis requires abdominal surgery that imposes significant physical burdens on dogs and cost burdens on owners. If cancer diagnosis can be conveniently made for companion animals such as dogs and cats, it would lead to early detection or precise diagnosis of cancer and would be expected to be useful for cancer therapy for companion animals. Also, if such convenient cancer diagnosis using serum becomes possible, it would be expected not only to enable cancer diagnosis but also to significantly contribute to periodic health examinations, preoperative diagnosis, and decisions about therapeutic strategy.

[0013] Health examination for companion animals, unlike the case of humans, is not prevalent. Hence, detection of cancer often occurs too late, such that an owner finds out the disease and then comes to a hospital only after the tumor has become large in many cases. If such tumor that has increased in size is malignant, it often results in treatment that is too late, even when surgical therapy such as surgery or medication using an anticancer agent or the like is performed. Hence, when a veterinarian determines that the tumor is malignant, anticancer agent treatment is generally performed without surgery. If surgery is performed, measures during surgery, such as determination of the size of margin to be secured, determination of the amount of blood required during surgery, and measures against cell scattering should also be strictly taken. It is desired that anticancer agent treatment is initiated immediately after surgery and that follow-up is performed at short intervals. Incorporation of the above cancer diagnosis into dog health checkups that are recently increasingly prevalent and are referred to as complete medical checkups for dogs is expected to lead to early cancer detection.

[0014] On the other hand, in the case of a benign tumor, surgery can be advised even if a tumor is large. After surgery, only resected areas need care without requiring any expensive anticancer agent treatment and without any need for apprehensions concerning follow-ups.

[0015] Under the current situation, provision of a convenient means for detecting cancer with high sensitivity, which is applicable to cancer diagnosis for animals, enables precise and efficient treatment and results in a number of advantages for both owners and veterinarians.

[0016] Cytoplasmic-and proliferation-associated protein 1 (CAPRIN-1) is an intracellular protein that is expressed when normal cells in resting phase are activated or undergo cell division. CAPRIN-1 is also known to be involved in mRNA transport through intracellular formation of intracellular stress grains with RNA and translation control, for example. Meanwhile, CAPRIN-1 has many different names. Examples of such names include GPI-anchored membrane protein 1 and membrane component surface marker 1 protein (M11S1), as if the protein has been known to be a membrane protein. These different names are derived from a report (J Biol Chem. 270: 20717-20723 (1995)) that the gene sequence of CAPRIN-1 originally has a GPI-binding region and CAPRIN-1 is a membrane protein expressed in large bowel-derived cell lines. It has been later reported that: the CAPRIN-1 gene sequence in this report is an error; frame shift takes place by deletion of 1 nucleotide from the CAPRIN-1 gene sequence currently registered with GenBank or the like, so that 80 amino acids are deleted from the C terminus and the resulting artifact (74 amino acids) corresponds to the GPI binding portion of the previous report; and an error is also present on the 5' side of the gene sequence and deletion of 53 amino acids from the N terminus has been proven (J Immunol. 172: 2389-2400 (2004)). Also, it has been reported that a protein encoded by the CAPRIN-1 gene sequence currently registered with GenBank or the like is not a cell membrane protein (J Immunol. 172: 2389-2400 (2004)).

[0017] In addition, based on the report of J Biol Chem. 270: 20717-20723 (1995) that CAPRIN-1 is a cell membrane

protein, US2008/0075722 and WO2005/100998 disclose that CAPRIN-1 under the name of M11S1 can be a target for cancer therapy as a cell membrane protein (not mentioned in the Examples). However, as reported in J Immunol. 172: 2389-2400 (2004), it has been accepted from the time of filing of US2008/0075722 and WO2005/100998 up to now that CAPRIN-1 is not expressed on cell surfaces. It is obvious that the content of US2008/0075722 and WO2005/100998 based only on misinformation to the effect that CAPRIN-1 is a cell membrane protein should not be understood as technical commonsense of persons skilled in the art. Moreover, it has never been reported that CAPRIN-1 is expressed at higher levels in breast cancer cells or the like than in normal cells.

SUMMARY OF THE INVENTION

PROBLEM TO BE RESOLVED BY THE INVENTION

[0018] An object of the present invention is to provide a means for detecting cancer that is useful for cancer diagnosis.

MEANS FOR RESOLVING THE PROBLEM

[0019] As a result of intensive studies, the present inventors have obtained cDNA encoding a protein that binds to an antibody existing in cancer-bearing living organism-derived serum by a SEREX method using a canine testis-derived cDNA library and the serum of a cancer-bearing dog, and thus they have prepared canine CAPRIN-1 proteins having the amino acid sequences shown in SEQ ID NOS: 6, 8, 10, 12, and 14 based on the cDNA. Also, the present inventors have prepared human CAPRIN-1 proteins having the amino acid sequences shown in SEQ ID NOS: 2 and 4 based on human genes homologous to the obtained genes. The present inventors have further discovered that: genes encoding these proteins are specifically expressed in canine and human testes and malignant cancer cells (see Example 1 described later); recombinant polypeptides prepared based on the amino acid sequences of these proteins specifically react only with sera from cancer-bearing living organisms; and CAPRIN-1 can be specifically detected from a cancer-bearing living organism using antibodies prepared using the recombinant polypeptides. Thus, the present inventors have completed that present invention.

[0020] Specifically, the present invention provides a method for detecting cancer comprising measuring CAPRIN-1 expression, which is performed for samples separated from living organisms. Also, the present invention provides a reagent for detecting cancer comprising an antibody that is induced *in vivo* against CAPRIN-1 and a polypeptide that undergoes an antigen-antibody reaction. Furthermore, the present invention provides a reagent for detecting cancer comprising an antibody that undergoes an antigen-antibody reaction with CAPRIN-1 or an antigen-binding fragment thereof. Furthermore, the present invention provides a reagent for detecting cancer comprising a polynucleotide that specifically hybridizes to a partial sequence of 15 or more nucleotides, preferably 20 to 25 or more nucleotides, and more preferably 30 or more nucleotides in the nucleotide sequence shown in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, or the like in the Sequence Listing.

[0021] Specifically, the present invention has the following characteristics.

(1) A method for detecting a cancer, comprising measuring the expression of a polypeptide having a reactivity of binding via an antigen-antibody reaction to an antibody against a CAPRIN-1 protein having any one of the amino acid sequences shown in the even-numbered SEQ ID NOS: 2-30 in the Sequence Listing, in a sample separated from a living organism.

(2) The method according to (1) above, wherein the polypeptide to be measured is a CAPRIN-1 protein having any one of the amino acid sequences shown in the even-numbered SEQ ID NOS: 2-30 (i.e., SEQ ID NOS: 2, 4, 6, 8,...30) or a polypeptide having 85% or more sequence identity with the CAPRIN-1 protein.

(3) The method according to (1) or (2) above, wherein the living organism is a human, a dog, or a cat.

(4) The method according to (3) above, wherein the living organism is a dog and the polypeptide to be measured has an amino acid sequence shown in any one of the even-numbered SEQ ID NOS: 2-30.

(5) The method according to (4) above, wherein the living organism is a dog and the polypeptide to be measured has the amino acid sequence shown in SEQ ID NO: 6, 8, 10, 12, or 14.

(6) The method according to (3) above, wherein the living organism is a human and the polypeptide to be measured has the amino acid sequence shown in SEQ ID NO: 2 or 4.

(7) The method according to any one of (1) to (6) above, wherein the expression of the polypeptide is measured by immunoassay of an antibody that can be contained in the sample and is induced *in vivo* against the polypeptide to be measured.

(8) The method according to any one of (1) to (7) above, wherein the sample is serum, blood plasma, ascite, or pleural effusion.

(9) The method according to any one of (1) to (6) above, wherein the expression of the polypeptide is measured by

measuring mRNA encoding the polypeptide, which is contained in the sample.

(10) The method according to (9) above, comprising examining the existing amount of the mRNA in the sample using a polynucleotide that specifically hybridizes to a partial sequence of 15 or more nucleotides, preferably 20 to 25 or more nucleotides, and more preferably 30 or more nucleotides in the nucleotide sequence of the above mRNA.

(11) The method according to (10) above, wherein the above living organism is a dog and the above polynucleotide is a polynucleotide specifically hybridizing to a partial sequence of 15 or more nucleotides, preferably 20 to 25 or more nucleotides, and more preferably 30 or more nucleotides in the nucleotide sequence shown in SEQ ID NO: 5, 7, 9, 11, or 13.

(12) The method according to (10) above, wherein the above living organism is a human and the above polynucleotide is a polynucleotide specifically hybridizing to a partial sequence of 15 or more nucleotides, preferably 20 to 25 or more nucleotides, and more preferably 30 or more nucleotides in the nucleotide sequence shown in SEQ ID NO: 1 or 3.

(13) The method according to any one of (9) to (12) above, wherein the above sample is a tissue or a cell.

(14) The method according to any one of (1) to (13) above, wherein the cancer is at least one type of cancer selected from the group consisting of brain tumor, squamous cell carcinoma of the head, neck, lung, uterus, or esophagus, melanoma, adenocarcinoma of the lung or uterus, renal cancer, malignant mixed tumor, hepatocellular carcinoma, basal cell carcinoma, acanthoma-like gingival tumor, tumor of the oral cavity, perianal adenocarcinoma, anal sac tumor, anal sac apocrine adenocarcinoma, sertoli cell carcinoma, cancer of vaginal vestibule, sebaceous adenocarcinoma, sebaceous epithelioma, sebaceous adenoma, sweat gland carcinoma, intranasal adenocarcinoma, nasal adenocarcinoma, thyroid cancer, large-bowel cancer, bronchial adenocarcinoma, adenocarcinoma, ductal carcinoma, breast adenocarcinoma, composite type breast adenocarcinoma, malignant mammary mixed tumor, intraductal papillary adenocarcinoma, fibrosarcoma, hemangiopericytoma, osteosarcoma, chondrosarcoma, soft tissue sarcoma, histiocytic sarcoma, myxosarcoma, undifferentiated sarcoma, lung cancer, mastocytoma, cutaneous leiomyoma, intraperitoneal leiomyoma, leiomyoma, chronic lymphocytic leukemia, lymphoma, gastrointestinal lymphoma, digestive lymphoma, small-cell-to-medium-cell lymphoma, adrenomedullary tumor, granulosa cell tumor, and pheochromocytoma.

(15) The method according to any one of (1) to (14) above, comprising further detecting the malignancy of cancer based on the fact that the malignancy of a cancer is high when the expression level of the above polypeptide is higher than that of a control.

(16) The method according to any one of (1) to (15) above, comprising further detecting the progression of cancer on the basis of the indicator that the extent of cancer is advanced when the expression level of the above polypeptide is higher than that of a control.

(17) A reagent for detecting a cancer, comprising a polypeptide that has a reactivity of binding via an antigen-antibody reaction to an antibody that is induced *in vivo* against a CAPRIN-1 protein having any one of the amino acid sequences shown in the even-numbered SEQ ID NOS: 2-30 in the Sequence Listing.

(18) A reagent for detecting a cancer, comprising an antibody or an antigen-binding fragment thereof that undergoes an antigen-antibody reaction with a polypeptide, wherein the polypeptide has a reactivity of binding via an antigen-antibody reaction to an antibody against a CAPRIN-1 protein having any one of the amino acid sequences shown in the even-numbered SEQ ID NOS: 2-30 in the Sequence Listing and is produced *in vivo* (or in a living body).

(19) The reagent for detecting cancer according to (18), wherein the antibody or antigen-binding fragment thereof that undergoes an antigen-antibody reaction with the polypeptide is an antibody or antigen-binding fragment thereof that binds to the surface of a cancer cell.

(20) The reagent for detecting cancer according to (18) or (19), wherein the antibody or antigen-binding fragment thereof that undergoes an antigen-antibody reaction with the polypeptide has an immunological reactivity with:

a polypeptide comprising an amino acid sequence of 7 or more continuous amino acid residues within the region of amino acid residue Nos. 50-98 or amino acid residue Nos. 233-305 in any one of the amino acid sequences shown in the even-numbered SEQ IDS NO: 2-30 excluding SEQ ID NO: 6 and SEQ ID NO: 18 or a polypeptide comprising the polypeptide as a partial sequence.

(21) The reagent for detecting a cancer according to any one of (18) to (20), wherein the antibody or antigen-binding fragment thereof that undergoes an antigen-antibody reaction with the polypeptide is an antibody or antigen-binding fragment thereof which binds to SEQ ID NO: 43, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 44 and 45, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 44 and 46, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 44 and 47, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 44 and 48, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 49 and 50, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 51 and 52, a monoclonal

antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 53 and 54, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 55 and 56, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 57 and 58, or a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 59 and 60.

(22) A reagent for detecting a cancer, comprising a polynucleotide that specifically hybridizes to a partial sequence of 15 or more nucleotides, preferably 20 to 25 or more nucleotides, and more preferably 30 or more nucleotides in any one of the nucleotide sequences shown in the odd-numbered SEQ ID NOS: 1-29 (i.e., SEQ ID NOS: 1, 3, 5, 7,...29) in the Sequence Listing.

ADVANTAGE OF THE INVENTION

[0022] According to the present invention, a new method for detecting a cancer is provided. As specifically described in Examples given later, a recombinant polypeptide prepared based on the amino acid sequence of CAPRIN-1 (or also referred to as Caprin-1) reacts with an antibody that specifically exists in the serum of a patient with cancer. Therefore, the cancer existing in a living body can be detected by measuring the antibody in a sample by the method of the present invention. Also, the cancer existing in a living body can be detected by measuring CAPRIN-1 itself. According to the method of the present invention, small-size cancer invisible to the naked eye or cancer in a deep part *in vivo* can be detected. Hence, the method of the present invention is useful for early detection of cancer at the time of health examination or the like. Furthermore, recurrent cancer can be detected early by the use of the method of the present invention for the follow-up of a patient after cancer treatment. Moreover, according to the method of the present invention, the extent of cancer can also be diagnosed, such as tumor increase, infiltration to the peripheral tissue, and cancer metastasis to a lymph node and a distant organ. Also, the serum antibody level is higher in a patient with highly malignant cancer than in a patient with low-malignant cancer. According to the method of the present invention, the malignancy of cancer can also be diagnosed. Also, as described in Examples below, mRNA encoding CAPRIN-1 is specifically expressed at high levels in testes and cancer cells. Therefore, cancers can also be detected by measuring the mRNA.

BRIEF DESCRIPTION OF THE DRAWINGS

[0023]

Fig. 1 shows the expression patterns of the gene encoding a CAPRIN-1 protein in normal tissues and tumor cell lines. Reference No. 1 indicates the expression patterns of the gene encoding the CAPRIN-1 protein. Reference No. 2 indicates the expression patterns of the GAPDH gene.

Fig. 2 shows the results of detecting by Coomassie staining the canine CAPRIN-1-derived polypeptide that is an example of polypeptides to be used in the present invention, which were produced and purified using *Escherichia coli* in the Examples. Reference No. 3 indicates the band of a canine CAPRIN-1-derived polypeptide.

Fig. 3 shows some of the results of cancer diagnosis for cancer-bearing dogs using the canine CAPRIN-1-derived polypeptides prepared in the Examples.

Fig. 4 shows some of the results of detailed cancer diagnosis for cancer-bearing dogs using the canine CAPRIN-1-derived polypeptides prepared in the Examples.

BEST MODE OF CARRYING OUT THE INVENTION

[0024] According to the method of the present invention, CAPRIN-1 expression is measured using a sample separated from a living organism. Examples of a method for measuring CAPRIN-1 expression include a method (1st method) that involves immunoassay for an antibody against CAPRIN-1 contained in a sample, a method (2nd method) that involves immunoassay for CAPRIN-1 itself contained in a sample, and a method (3rd method) that involves measurement of mRNA encoding CAPRIN-1 contained in a sample. In the method of the present invention, CAPRIN-1 expression may be measured by any of these methods. In the present invention, the term "measurement" refers to any of detection, qualitative determination, quantitative determination, and semi-quantitative determination.

[0025] The amino acid sequence shown in SEQ ID NO: 6, 8, 10, 12, or 14 is the amino acid sequence of canine CAPRIN-1. Canine CAPRIN-1 having the amino acid sequence was identified as a polypeptide binding to an antibody specifically existing in the cancer-bearing dog-derived serum by the SEREX method using a canine testis-derived cDNA library and the serum of a cancer-bearing dog (see Example 1). Specifically, an antibody against CAPRIN-1 having the amino acid sequence shown in SEQ ID NO: 6, 8, 10, 12, or 14 is specifically induced *in vivo* in a cancer-bearing dog. Therefore, canine cancer can be detected by measuring the above antibody against CAPRIN-1 having the amino acid sequence shown in SEQ ID NO: 6, 8, 10, 12, or 14 using the above 1st method (see Examples 3 and 4). Canine cancer

can also be detected by measuring CAPRIN-1 itself as an antigen shown in SEQ ID NO: 6, 8, 10, 12, or 14 using the above 2nd method (see Examples 5 and 6). Also, canine cancer can be detected, as described in the following Examples, by measuring mRNA encoding CAPRIN-1 since the mRNA is expressed at significantly high levels in testes and cancer cells (see Example 1).

[0026] The term "having an amino acid sequence" as used herein refers to amino acid residues being aligned in the relevant order. Therefore, for example, the expression "polypeptide having the amino acid sequence shown in SEQ ID NO: 2" refers to a polypeptide having 709 amino acid residues, which consists of the amino acid sequence of Met Pro Ser Ala... (abbreviated)... Gln Gln Val Asn shown in SEQ ID NO: 2. Also, for example, the expression "polypeptide having the amino acid sequence shown in SEQ ID NO: 2" may also be abbreviated as "the polypeptide of SEQ ID NO: 2." The same applies to the expression "having a/the nucleotide sequence." In this case, the term "having" may be substituted with the expressions "consisting of."

[0027] Also, the term "polypeptide" as used herein refers to a molecule that is formed via peptide bonding of a plurality of amino acids. Examples of such molecule include not only polypeptide molecules with a large number of constituent amino acids, but also low-molecular-weight molecules (oligopeptides) with small number of amino acids and full-length proteins. The present invention further encompasses full-length CAPRIN-1 proteins each having an amino acid sequence shown in an even-numbered sequence ID from among SEQ ID NOS: 2-30.

[0028] In the method of the present invention, not only canine CAPRIN-1 of SEQ ID NO: 6, 8, 10, 12, or 14, but also CAPRIN-1 of other mammals (hereinafter, may also be referred to as "homolog" for canine CAPRIN-1. When simply referred to as "CAPRIN-1," CAPRIN-1 from not only a dog but also from another mammal is also encompassed herein) are also subjected to measurement. As specifically described in the following Examples, mRNA encoding human CAPRIN-1 is significantly expressed at a high level in human testis and cancer cells, as in the case of canine CAPRIN-1 of SEQ ID NO: 6, 8, 10, 12 or 14. However, no antibody against the human CAPRIN-1 is detected in a healthy human body. Also, an antibody against feline CAPRIN-1 is not detected in a healthy cat body, but is detected in a cancer-bearing cat alone. Therefore, cancer of a mammal other than a dog can be detected by measuring CAPRIN-1 expression in the mammal. Examples of CAPRIN-1 of mammals other than dogs, which are measurement subjects in the method of the present invention, include, but are not limited to, human CAPRIN-1 and feline CAPRIN-1. A nucleotide sequence encoding human CAPRIN-1 and the amino acid sequence thereof are as separately shown in SEQ ID NO: 1 and 3, and 2 and 4, respectively, in the Sequence Listing. Sequence identity with canine CAPRIN-1 is 94% in terms of nucleotide sequence and is 98% in terms of amino acid sequence. Even dogs and humans which are genetically distant mammals share as very high as 98% sequence identity in terms of the amino acid sequence of CAPRIN-1. Therefore, it is thought that a dog and a mammal other than a human; that is, canine CAPRIN-1 and homolog thereof share sequence identity as high as about 85% or more. Therefore, CAPRIN-1, the expression of which is measured in the method of the present invention, has preferably 85% or more and more preferably 95% or more sequence identity with the amino acid sequence of canine CAPRIN-1 shown in SEQ ID NO: 6, 8, 10, 12, or 14. However, such examples are not particularly limited thereto.

[0029] In the 1st method above, the above antibody that can be present in a sample can be easily measured by immunoassay using an antigenic substance that undergoes an antigen-antibody reaction with the antibody. Immunoassay itself is a known conventional method as specifically described below. As an antigenic substance for immunoassay, the canine CAPRIN-1 of SEQ ID NO: 6, 8, 10, 12, or 14 that causes the induction of the antibody within a cancer-bearing dog body can be used. Furthermore, an antibody has cross-reactivity. Thus, even a molecule other than an antigenic substance actually having served as an immunogen can bind to an antibody induced against the immunogen via an antigen-antibody reaction, as long as a structure analogous to the epitope of the immunogen is present on the molecule. In particular, a protein from a mammal and homolog thereof from another mammal share high amino acid sequence identity and often have epitope structures analogous to each other. As specifically described in the following Examples, the canine CAPRIN-1 of SEQ ID NO: 6, 8, 10, 12, or 14 undergoes an antigen-antibody reaction not only with an antibody induced against the canine CAPRIN-1 within a cancer-bearing dog body, but also with an antibody induced against feline CAPRIN-1 within a cancer-bearing cat body. Moreover, human CAPRIN-1 undergoes an antigen-antibody reaction with the above antibody induced within cancer-bearing dog or cancer-bearing cat bodies. Accordingly, in the 1st method of the present invention, CAPRIN-1 from any mammal can be used as an antigen for immunoassay.

[0030] In general, when an antigenic substance is a protein or the like having a complicated structure and high molecular weight, a plurality of sites having different structures are present on the molecule. Therefore, a plurality of types of antibody capable of recognizing and binding to different sites of such antigenic substances are produced *in vivo*. Specifically, an antibody that is produced *in vivo* against an antigenic substance such as protein is a polyclonal antibody that is a mixture of a plurality of types of antibody. An antibody discovered by the present inventors is also a polyclonal antibody. It is specifically present in cancer-bearing living organism-derived serum and specifically binds to a recombinant CAPRIN-1 protein via an antigen-antibody reaction. The term "polyclonal antibody" used in the present invention refers to an antibody that exists in serum from a living organism containing an antigenic substance therein and is induced *in vivo* against the antigenic substance.

[0031] In Examples described later, polypeptides of SEQ ID NO: 6 and SEQ ID NO: 8 (canine CAPRIN-1) and the

polypeptide of SEQ ID NO: 2 (human CAPRIN-1) were prepared as antigens for immunoassay of specific antibodies in the cancer-bearing living animals. Then reactivity between these polypeptides and the above antibody in serum from a cancer-bearing living organism was confirmed. However, the above antibody is a polyclonal antibody, so that it naturally binds to a polypeptide consisting of the homolog of SEQ ID NO: 6, 8, or 2. Even in the case of a fragment of said polypeptides, it can bind to the above antibody contained in serum from a cancer-bearing living organism, since the polyclonal antibody can contain an antibody capable of recognizing the structure of the relevant fragment. That is, either a polypeptide (that is, full-length CAPRIN-1 protein) of the homolog of SEQ ID NO: 6, 8, or 2 or a fragment thereof can be similarly used for measurement of the above polyclonal antibody contained specifically in serum of a cancer-bearing living organism and is useful for cancer detection. Therefore, examples of a polypeptide to be used as an antigen for immunoassay in the 1st method of the present invention include, not only a polypeptide that consists of the full-length region of CAPRIN-1 (e.g., SEQ ID NO: 6, 8, or 2), but also a polypeptide fragment that consists of continuous 7 or more, preferably continuous 8 or more, 9 or more, or 10 or more amino acids in the amino acid sequence of CAPRIN-1 and undergoes an antigen-antibody reaction with a polyclonal antibody against CAPRIN-1 (hereinafter, may be conveniently referred to as "a specifically reactive partial polypeptide"). It is known in the art that a polypeptide of about 7 or more amino acid residues exerts antigenicity. However, if the number of amino acid residues constituting a polypeptide is too low, such polypeptide highly likely cross-reacts with antibodies, which exist in the sample, against proteins other than CAPRIN-1. Accordingly, in view of increasing the accuracy of immunoassay, the desirable number of amino acid residues of a polypeptide fragment may be preferably 30 or more or 50 or more, further preferably 100 or more or 150 or more, further preferably 300 or more, even more preferably 600 or more, and further preferably 1000 or more and 1500 or more.

[0032] Specific preferable examples of the polypeptides to be used as antigens are the polypeptides of the even-numbered SEQ ID NOS: 2-30 or fragments thereof.

[0033] Nucleotide sequences of polynucleotides encoding proteins consisting of the amino acid sequences of the even-numbered SEQ ID NOS: 2-30 (that is, SEQ ID NOS: 2, 4, 6...28, 30) are shown in the odd-numbered SEQ ID NOS: 1-29 (that is, SEQ ID NOS: 1, 3, 5...27, 29).

[0034] In general, it is broadly known by persons skilled in the art concerning protein antigens such that even when few amino acid residues have been substituted, deleted, added, or inserted in the amino acid sequence of the protein, the resultant may retain antigenicity almost equivalent to that of the original protein. Therefore, a polypeptide: having a sequence that has a substitution, a deletion, and/or an insertion of a few (preferably one or several) amino acid residues with respect to the amino acid sequence of CAPRIN-1 and has 80% or more, 85% or more, preferably 90% or more, more preferably 95% or more, and further preferably 98% or more sequence identity with the original sequence; and specifically binding to a polyclonal antibody against CAPRIN-1 via an antigen-antibody reaction (hereinafter, may be conveniently referred to as "specifically reactive modified polypeptide") can be used for cancer detection in a manner similar to that for the above polypeptides. Preferably, the specifically reactive modified polypeptide has an amino acid sequence that has a substitution, a deletion, an addition, and/or an insertion of one or several amino acid residues with respect to the amino acid sequence of CAPRIN-1. The term "several" as used herein refers to an integer of 2-10, preferably an integer of 2-6, and further preferably an integer of 2-4.

[0035] The term "sequence identity (of amino acid sequences)" as used herein is obtained by aligning two amino acid sequences to be compared so that amino acid residues match as many as possible, subtracting the number of amino acid residues that have matched from the total number of amino acid residues, and then expressing the result in percentage form. Upon the above alignment, if necessary, gaps are appropriately inserted into one of or both sequences to be compared. Such sequence alignment can be performed using a known program such as BLAST, FASTA, or CLUSTAL W (Karlin and Altschul, Proc. Natl. Acad. Sci. U.S.A., 87: 2264-2268, 1993; Altschul et al., Nucleic Acids Res., 25: 3389-3402, 1997).

[0036] Twenty types of amino acid constituting natural proteins can be grouped into neutral amino acids having side chains with low polarity (Gly, Ile, Val, Leu, Ala, Met, and Pro), neutral amino acids having hydrophilic side chains (Asn, Gln, Thr, Ser, Tyr, and Cys), acidic amino acids (Asp and Glu), basic amino acids (Arg, Lys, and His), and aromatic amino acids (Phe, Tyr, Trp, and His) in which the members of each group have properties analogous to each other. It is known that substitution among these amino acids (that is, conservative substitution) rarely alters the properties of the resulting polypeptide. Therefore, when amino acid residues of CAPRIN-1 are substituted, substitution is performed between members of the same group so that a possibility of maintaining binding with the corresponding antibody becomes higher. However, in the present invention, the above variant may involve non-conservative substitution, as long as immune-inducing activity equivalent to or almost equivalent to that of a non-variant is imparted.

[0037] A polypeptide (hereinafter, may conveniently be referred to as "specifically reactive addition polypeptide") that contains as a partial sequence the above polypeptide to be used in the present invention (that is, prepared by addition of another (poly)peptide to one end or both ends of a polypeptide to be used in the present invention) and specifically binds to a polyclonal antibody against CAPRIN-1 via an antigen-antibody reaction can also be used for cancer detection in a manner similar to that for the above polypeptides.

[0038] The above polypeptides to be used in the present invention can be synthesized according to a chemical synthesis

method such as an Fmoc method (fluorenylmethyloxycarbonyl method) and a tBoc method (t-butyloxy-carbonyl method) (Ed., The Japanese Biochemical Society, Seikagaku Jikken Koza (Biochemical Experimental Lecture Series) 1, Protein Chemistry IV, Chemical Modification and Peptide Synthesis, TOKYO KAGAKU DOZIN CO., LTD (Japan), 1981). Also, the polypeptides can also be synthesized by a conventional method using various commercially available peptide synthesizers. Alternatively, the polypeptides can be easily prepared using known genetic engineering techniques (Sambrook et al., Molecular Cloning, 2nd Edition, Current Protocols in Molecular Biology (1989), Cold Spring Harbor Laboratory Press, Ausubel et al., Short Protocols in Molecular Biology, 3rd Edition, A Compendium of Methods from Current Protocols in Molecular Biology (1995), John Wiley & Sons, and the like). For example, from RNA extracted from a tissue expressing a gene encoding the human CAPRIN-1 of SEQ ID NO: 2 or a homolog thereof, cDNA of the gene is prepared by RT-PCR. The full-length sequence or a desired partial sequence of the cDNA is incorporated into an expression vector and then the vector is introduced into host cells, so that a polypeptide of interest can be obtained. The nucleotide sequences of cDNAs encoding canine CAPRIN-1 of SEQ ID NOS: 6, 8, 10, 12, and 14 are shown in SEQ ID NOS: 5, 7, 9, 11, and 13, respectively. The human factors homolog thereof; that is, the nucleotide sequences of cDNAs encoding human CAPRIN-1 of SEQ ID NOS: 2 and 4 are shown in SEQ ID NOS: 1 and 3, respectively. Hence, primers to be used for RT-PCR can be easily designed in reference to these nucleotide sequences. Also, as described later, a gene encoding CAPRIN-1 of a non-human mammal can be amplified using primers designed in reference to the nucleotide sequences of the odd-numbered SEQ ID NOS: 1-29. For example, cDNA encoding feline CAPRIN-1 can be easily prepared by techniques similar to the above techniques. RNA extraction, RT-PCR, cDNA incorporation into a vector, and introduction of a vector into host cells can be performed by known methods as described below, for example. Also, vectors and host cells to be used herein are also known and various vectors and host cells are commercially available.

[0039] The above host cells may be any cells, as long as they can express the above polypeptides. Examples of prokaryotic host cells include *Escherichia coli* and the like. Examples of eukaryotic host cells include mammalian cultured cells such as monkey kidney cells (COS1), Chinese hamster ovary cells (CHO), the human embryonic kidney cell line (HEK293), and the mouse embryonic skin cell line (NIH3T3), budding yeast, fission yeast, silkworm cells, and *Xenopus* oocytes.

[0040] When prokaryotic cells are used as host cells, an expression vector having a replication origin in prokaryotic cells, a promoter, a ribosome-binding site, a multi-cloning site, a terminator, a drug-resistance gene, an auxotrophic complementary gene, and the like are used. As expression vectors for *Escherichia coli*, pUC vectors, pBluescriptII, pET expression systems, pGEX expression systems, and the like can be exemplified. A DNA encoding the above polypeptide is incorporated into such an expression vector, prokaryotic host cells are transformed with the vector, and then the thus obtained transformant is cultured, so that the polypeptide encoded by the DNA can be expressed in the prokaryotic host cells. At this time, the polypeptide can also be expressed as a fusion protein with another protein. A DNA encoding the above polypeptide can be obtained by preparing a cDNA by RT-PCR as described above, for example. Moreover, such DNA encoding the above polypeptide can be also synthesized by a conventional method using a commercially available nucleic acid synthesizer as described below. The nucleotide sequences of cDNAs of the genes encoding CAPRIN-1 of SEQ ID NOS: 2 and 4 are shown in SEQ ID NOS: 1 and 3, respectively, in the Sequence Listing.

[0041] When eukaryotic cells are used as host cells, expression vectors for eukaryotic cells having a promoter, a splicing region, a poly(A) additional site, and the like are used. Examples of such expression vectors include pKA1, pCDM8, pSVK3, pMSG, pSVL, pBK-CMV, pBK-RSV, EBV vector, pRS, pcDNA3, and pYES2. Similarly to the above, a DNA encoding a polypeptide to be used in the present invention is incorporated into such an expression vector, eukaryotic host cells are transformed with the vector, and then the thus obtained transformant is cultured, so that the polypeptide encoded by the above DNA can be expressed in eukaryotic host cells. When pIND/V5-His, pFLAG-CMV-2, pEGFP-N1, pEGFP-C1, or the like is used as an expression vector, the above polypeptide can be expressed as a fusion protein with various tags, such as a His tag (e.g., (His)₆ to (His)₁₀), a FLAG tag, a myc tag, a HA tag, and GFP.

[0042] For introduction of an expression vector into a host cell, known methods can be employed such as electroporation, a calcium phosphate method, a liposome method, a DEAE dextran method, microinjection, viral infection, lipofection, and binding with a cell-membrane-permeable peptide.

[0043] Isolation and purification of a polypeptide of interest from host cells can be performed using known isolation techniques in combination. Examples of such known techniques include treatment using a denaturing agent such as urea or a surfactant, ultrasonication, enzymatic digestion, salting-out, solvent fractionation and precipitation, dialysis, centrifugation, ultrafiltration, gel filtration, SDS-PAGE, isoelectric focusing, ion exchange chromatography, hydrophobic chromatography, affinity chromatography, and reverse phase chromatography.

[0044] Polypeptides obtained by the above methods include polypeptides in the form of fusion proteins with any other proteins. An example of such a fusion protein include a fusion protein with glutathione-S-transferase (GST), a His tag, or the like. Polypeptides in the form of such fusion proteins are also examples of the above-described specifically reactive addition polypeptides and can be used for the 1st detection method of the present invention. Furthermore, a polypeptide expressed in transformed cells may be subjected to various types of modification within cells after translation. Such polypeptide that is modified after translation can be used in the 1st detection method of the present invention, as long

as it is capable of binding to a polyclonal antibody against CAPRIN-1. Examples of such post-translation modification include the removal of N-terminal methionine, N-terminal acetylation, glycosylation, limited proteolysis by intracellular protease, myristoylation, isoprenylation, and phosphorylation.

[0045] An antibody in a sample can be easily measured by immunoassay using the above polypeptide as an antigen. Immunoassay itself is known in the art. Immunoassay is classified into a sandwich method, a competition method, an agglutination method, Western blot method, and the like based on types of reaction. Also, immunoassay is classified based on labels into radioimmunoassay, fluorescence immunoassay, enzyme immunoassay, and biotin immunoassay, for example. Immunoassay of the above antibody can be performed using any of these methods. Sandwich ELISA or the agglutination method are preferably applicable as an immunoassay technique for the above antibody in the method of the present invention, since the procedures of these methods are convenient and require no extensive apparatus and the like. But the techniques are not limited to them. When an enzyme is used as a label for an antibody, such enzyme is not particularly limited, as long as it satisfies conditions such that: the turn over number is high; it remains stable even if it is bound to an antibody, it specifically causes the color development of the substrate, and the like. Examples of enzymes that can be used for general enzyme immunoassay include peroxidase, β -galactosidase, alkaline phosphatase, glucose oxidase, acetylcholine esterase, glucose-6-phosphorylation dehydrogenase, and malic acid dehydrogenase. Also, enzyme-inhibiting substances, coenzymes, and the like can be used. Binding of these enzymes with antibodies can be performed by known methods using a cross-linking agent such as a maleimide compound. As a substrate, a known substance can be used depending on the type of an enzyme to be used. For example, when peroxidase is used as an enzyme, 3,3',5,5'-tetramethylbenzidine can be used. Also when alkaline phosphatase is used as an enzyme, para-nitrophenol or the like can be used. As a radio isotope, a radio isotope that is generally used for radioimmunoassay, such as ^{125}I and ^3H can be used. As a fluorescent dye, a fluorescent dye that is used for general fluorescent antibody techniques, such as fluorescence isothiocyanate (FITC) and tetramethylrhodamine isothiocyanate (TRITC) can be used.

[0046] There is no need to explain the above immunoassay techniques in the Description, since they are well-known. However, when these immunoassay techniques are briefly described, the sandwich method involves immobilizing the above polypeptide to be used as an antigen to a solid phase, reacting it with a sample such as serum, washing, reacting with an appropriate secondary antibody, washing, and then measuring the secondary antibody bound to the solid phase, for example. An unbound secondary antibody can be easily removed by immobilization of an antigen polypeptide to a solid phase. Hence, this is preferable as an embodiment of the method for detecting cancer of the present invention. As a secondary antibody, an anti-canine IgG antibody can be used if a sample is derived from a dog. A secondary antibody is labeled in advance with a labeling substance exemplified above, so that the secondary antibody binding to a solid phase can be measured. The thus measured amount of the secondary antibody corresponds to the amount of the above antibody in the serum sample. When an enzyme is used as a labeling substance, the amount of the antibody can be measured by adding a substrate that is digested to develop color by enzymatic action and then optically measuring the amount of the substrate degraded. When a radio isotope is used as a labeling substance, the amount of radiation from the radio isotope can be measured using a scintillation counter or the like.

[0047] In the 2nd method of the present invention, CAPRIN-1 that can be contained in a sample from a living organism is measured. As described above, among cancer patients, the amount of an antibody that undergoes an antigen-antibody reaction with CAPRIN-1 of a dog, a human, or the like is significantly high. This indicates that the amount of CAPRIN-1 accumulated as an antigen is significantly high in cancer cells. Cancer can also be detected by directly measuring CAPRIN-1, as specifically described in Examples below. Therefore, cancer can be detected *in vivo* by measuring CAPRIN-1 itself similarly to the 1st method above.

[0048] A polypeptide in a sample can be easily measured by well-known immunoassay techniques. Specifically, for example, an antibody or an antigen-binding fragment thereof, which undergoes an antigen-antibody reaction with CAPRIN-1, is prepared, immunoassay is performed using the antibody or its antigen-binding fragment thereof, and then CAPRIN-1 that may be present in the sample can be measured. As described above, an antibody has cross-reactivity. Hence, for example, through the use of an antibody or the antigen-binding fragment thereof, which undergoes an antigen-antibody reaction with the canine CAPRIN-1 of SEQ ID NO: 6, not only the canine CAPRIN-1 of SEQ ID NO: 6, but also its homolog in other mammals (e.g., the human CAPRIN-1 of SEQ ID NO: 2 or 4 and feline CAPRIN-1) can be measured. An immunoassay technique itself is a known conventional technique as described above.

[0049] This examination revealed that CAPRIN-1 is a cell membrane protein that is expressed on the surfaces of cancer cells. A living organism with cancer contains many kinds of proteases. Specifically, in a living organism with cancer, an extracellularly expressed portion of the CAPRIN-1 sequence is separated from the cancer cells by degradation, so that such portion exists at a level higher than an intracellularly expressed portion of the CAPRIN-1 sequence. Therefore, when an antibody against CAPRIN-1 or an antigen-binding fragment thereof to be used in this measurement, which binds to the surface of the cancer cell, is used, CAPRIN-1 can be detected at higher levels and cancer can be diagnosed with higher sensitivity. Therefore, in the present invention, antibodies binding to a portion of the CAPRIN-1 protein existing on the surfaces of cancer cells, are preferably used. An example of a partial peptide of the CAPRIN-1 protein existing on the surfaces of cancer cells, is a polypeptide comprising a sequence of continuous 7 or more amino acid residues

within the region of amino acid residue Nos. (aa) 50-98 or amino acid residue Nos. (aa) 233-305 in the amino acid sequences shown in the even-numbered SEQ ID NOS: 2-30 in the Sequence Listing excluding SEQ ID NO: 6 and SEQ ID NO: 18. A specific example thereof is the amino acid sequence shown in SEQ ID NO: 43 or SEQ ID NO: 61 (in the amino acid sequence shown in SEQ ID NO: 61, a region of the amino acid sequence shown in SEQ ID NO: 62 or SEQ ID NO: 63 is preferred) or an amino acid sequence having 80% or more, preferably 85% or more, more preferably 90% or more, further preferably 95% or more sequence identity with the relevant amino acid sequence. Examples of an antibody to be used in the present invention include all antibodies binding to these peptides. Specific examples of the antibody include an antibody or antigen-binding fragment thereof which binds to SEQ ID NO: 43, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 44 and 45, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 44 and 46, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 44 and 47, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 44 and 48, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 49 and 50, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 51 and 52, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 53 and 54, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 55 and 56, a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 57 and 58, or a monoclonal antibody or antigen-binding fragment thereof having the amino acid sequences of SEQ ID NOS: 59 and 60.

[0050] The term "antigen-binding fragment" as used herein refers to an antibody fragment capable of binding to an antigen such as a Fab fragment and a $F(ab')_2$ fragment contained in an antibody molecule. An antibody to be used herein may be a polyclonal antibody or a monoclonal antibody. For immunoassay and the like, a monoclonal antibody with high reproducibility is preferable. A method for preparing a polyclonal antibody and a monoclonal antibody using a polypeptide as an immunogen is known and can be easily performed by a conventional method. For example, CAPRIN-1 is bound to a carrier protein such as keyhole limpet hemocyanin (KLH), casein, or serum albumin and then an animal is immunized with the resultant as an immunogen together with an adjuvant, and thereby an antibody against CAPRIN-1 can be induced. Antibody-producing cells such as splenocytes or lymphocytes collected from the immunized animal are fused to myeloma cells to prepare hybridomas, and then hybridomas producing an antibody that binds to CAPRIN-1 are selected and then grown, so that a monoclonal antibody, whose the corresponding antigen is CAPRIN-1, can be obtained from the cultured supernatant. The above method is a known conventional method.

[0051] In the 3rd method of the present invention, mRNA encoding CAPRIN-1 that can be contained in a sample obtained from a living organism is measured. As specifically described in Examples below, mRNA encoding the canine CAPRIN-1 of SEQ ID NO: 6, 8, 10, 12, or 14 or human CAPRIN-1 of SEQ ID NO: 2 or 4 is expressed at a significantly high level in cancer cells. Therefore, cancer can be detected *in vivo* by measuring such mRNA in a sample.

[0052] mRNA in a sample can be quantitatively determined by a conventional method such as real-time detection RT-PCR using the mRNA as a template, for example. Such mRNA can generally be quantitatively determined based on staining intensity or the like in Northern blot that is a conventional method. The cDNA sequences encoding CAPRIN-1 polypeptides of the even-numbered SEQ ID NOS: 2-30 are shown in the odd-numbered SEQ ID NOS: 1-29, respectively. Hence, based on these sequences, a polynucleotide specifically hybridizing to a partial region in the nucleotide sequence shown in any of the odd-numbered SEQ ID NOS: 1-29 (hereinafter, referred to as "polynucleotide for cancer detection") is prepared and then the amount of the mRNA in a sample can be measured using the polynucleotide as a probe or a primer for a nucleic acid amplification method. As described later, if it is a polynucleotide specifically hybridizing to a partial region in the nucleotide sequence shown in any of the odd-numbered SEQ ID NOS: 1-29, mRNA encoding CAPRIN-1 in mammals other than dogs and humans can also be determined. In addition, in the present invention, a polynucleotide may be RNA or DNA.

[0053] The term "specifically hybridizing to" as used herein refers to that under general hybridization conditions, a subject hybridizes to only a target partial region, but does not substantially hybridize to the other regions.

[0054] The term "(under) general hybridization conditions" as used herein refers to conditions employed for annealing in general PCR or detection using a probe. For example, in the case of PCR using Taq polymerase, the term refers to conditions under which a reaction is performed at an appropriate annealing temperature ranging from about 54°C to 60°C using a general buffer such as 50 mM KCl, 10 mM Tris-HCl (pH8.3-9.0), and 1.5 mM MgCl₂. Also, in the case of Northern hybridization, for example, the term refers to conditions under which a reaction is performed using a general hybridization solution such as 5 × SSPE, 50% formamide, 5 × Denhardt's solution, and 0.1% SDS-0.5% SDS, or 0.1-5 × SSC and 0.1-0.5% SDS at an appropriate hybridization temperature ranging from about 42°C to 65°C. Furthermore, after hybridization, washing is performed with 0.1-0.2 × SSC and 0.1% SDS, for example. However, appropriate annealing temperatures or hybridization temperatures are not limited to the above examples, and are determined based on T_m value for a polynucleotide for cancer detection, which is used as a primer or a probe, and the empirical rule of experimenters. Persons skilled in the art can easily determine such temperature range.

[0055] The expression "does not substantially hybridize to" as used herein refers to that a subject does not really

hybridize to a target partial region or a subject hybridizes to a target partial region in a significantly low amount; that is, in a relatively negligibly-small amount, even when it hybridizes to the target partial region. An example of a polynucleotide specifically hybridizing under such conditions is a polynucleotide having sequence identity at a level or more with the nucleotide sequence of a target partial region. A specific example of such polynucleotide has 70% or more, preferably 80% or more, 85% or more, more preferably 90% or more, further preferably 93% or more, further preferably 95% or more, and further more preferably 98% or more sequence identity. Most preferably, the polynucleotide has a nucleotide sequence identical to the nucleotide sequence of a target partial region. Sequence identity is defined in the same manner as that for the sequence identity of the above amino acid sequence. Even if a terminus of a polynucleotide for cancer detection contains a region not hybridizing to a subject, in the case of a probe, it can be used for detection as long as a hybridizing region occupies as much as about a half or more of the entire probe. Also, in the case of a primer, it can be used for detection as long as a hybridizing region occupies as much as about a half or more of the entire primer and is located on the 3' terminal side, since normal annealing and extension reaction can take place. As described above, when a terminus of a polynucleotide for cancer detection contains a non-hybridizing region, sequence identity with a target nucleotide sequence is calculated focusing on only a hybridizing region without taking non-hybridizing region into consideration.

[0056] The term "partial sequence" in the present invention refers to a partial sequence in the nucleotide sequences shown in the odd-numbered SEQ ID NOS: 1-29, specifically the partial sequence having a sequence of continuous 15 or more nucleotides, preferably continuous 18 or more nucleotides, more preferably continuous 20 or more nucleotides or 25 or more nucleotides, and further preferably continuous 30, 40, or 50 or more nucleotides. The expression "the nucleotide sequence shown in SEQ ID NO: 5" as used herein refers to, in addition to the nucleotide sequence actually shown in SEQ ID NO: 5, a sequence complementary to the sequence. Therefore, for example, the expression "a polynucleotide having the nucleotide sequence shown in SEQ ID NO: 5" refers to a single-stranded polynucleotide having the nucleotide sequence actually shown in SEQ ID NO: 5, a single-stranded polynucleotide having a nucleotide sequence complementary to that shown in SEQ ID NO: 5, and a double-stranded polynucleotide comprising them. When a polynucleotide to be used in the present invention is prepared or a polynucleotide encoding a polypeptide to be used in the present invention is prepared, any one nucleotide sequence is appropriately selected and this selection can be easily performed by persons skilled in the art.

[0057] The number of nucleotides in a polynucleotide for cancer detection is preferably 18 or more nucleotides in view of ensuring specificity. When used as a probe, the size of the polynucleotide is preferably 18 or more nucleotides, is further preferably 20 or more nucleotides and the full-length or less of the coding region. When used as a primer, the size of the polynucleotide is preferably 18 or more nucleotides and 50 or less nucleotides. A preferred example of the polynucleotide for cancer detection is a polynucleotide comprising continuous 18 or more nucleotides in a nucleotide sequence shown in any of the odd-numbered SEQ ID NOS: 1-29.

[0058] It is obvious for persons skilled in the art who refer this Description that: a polynucleotide specifically hybridizing to a partial region in SEQ ID NO: 5, 7, 9, 11, or 13 is used for measurement of the amount of mRNA encoding the canine CAPRIN-1 of SEQ ID NO: 6, 8, 10, 12, or 14, respectively; and a polynucleotide specifically hybridizing to a partial region in SEQ ID NO: 1 or 3 is used for measurement of the amount of mRNA encoding the human CAPRIN-1 of SEQ ID NO: 2 or 4, respectively. However, a protein from a mammal and a homolog thereof from another mammal generally share high sequence identity even at the nucleotide sequence level. Thus, the sequence identity among the sequences of the odd-numbered SEQ ID NOS: 1-13 also is as very high as 94% to 100%. Accordingly, a polynucleotide specifically hybridizing to a partial region of the sequence of SEQ ID NO: 5 can also specifically hybridize to a partial region corresponding to the relevant partial region of any of the odd-numbered SEQ ID NOS: 1-29.

[0059] Actually as described in Examples below, a pair of primers having the nucleotide sequences shown in SEQ ID NO: 33 and 34, respectively, specifically hybridizes to both a partial region of any of the sequences of the odd-numbered SEQ ID NOS: 1-29 and a partial region of the sequence of SEQ ID NO: 5, so that both mRNA encoding the canine CAPRIN-1 of SEQ ID NO: 6 and mRNA encoding a homolog thereof can be measured, for example. Accordingly, for example, with the use of a polynucleotide specifically hybridizing to a partial region of the sequence of SEQ ID NO: 5, not only mRNA encoding the canine CAPRIN-1 of SEQ ID NO: 6, but also mRNA encoding the human CAPRIN-1 of SEQ ID NO: 2 or 4 can be measured. Similarly, a mRNA encoding CAPRIN-1 of another mammal such as a cat can also be measured. When a polynucleotide for cancer detection is designed, it is desirable to select partial regions having a specifically high sequence identity between the SEQ ID numbers (odd-numbered SEQ ID NOS: 1-29) (preferably, the nucleotide sequences are the same). If a partial region having particularly high sequence identity between a dog and a human is present, a region having very high sequence identity with the region is expected to be present in a homologous gene of another animal species. Through selection of such partial regions, accuracy for measuring mRNA encoding CAPRIN-1 of an animal species other than dogs and humans can be increased.

[0060] A method itself for measuring a test nucleic acid using a polynucleotide specifically hybridizing to a partial region of the test nucleic acid as a primer or a probe for a nucleic acid amplification method such as PCR is well-known. Examples of such method include, in addition to RT-PCR that is specifically described in Examples below, Northern blot

and In situ hybridization. When the amount of mRNA is measured in the present invention, all of these known measuring methods can be employed.

[0061] A nucleic acid amplification method itself such as PCR is well-known in the art and thus reagent kits and apparatuses therefor are commercially available, so that the method can be easily performed. Specifically, for example, denaturation, annealing, and extension steps are each performed using a test nucleic acid (e.g., the cDNA of a gene encoding a protein having an amino acid sequence shown in any of the even-numbered SEQ ID NOS: 2-30) as a template and a pair of polynucleotides (primers) for cancer detection in a known buffer in the presence of thermostable DNA polymerase such as Taq polymerase or Pfu polymerase and dNTP (here, N =

[0062] A, T, C, or G) by varying the temperature of the reaction solution. In general, the denaturation step is performed at 90°C-95°C, the annealing step is performed at or near the T_m of the template and the primers (preferably within $\pm 4^\circ\text{C}$), and the extension step is performed at 72°C which is an optimum temperature for thermostable DNA polymerase such as Taq polymerase or Pfu polymerase or a temperature near the optimum temperature. Each step is performed for about 30 seconds to 2 minutes, as appropriately selected. This heating cycle is repeated about 25 to 40 times, for example, so that the template nucleic acid region flanked by a primer pair is amplified. A nucleic acid amplification method is not limited to PCR and any other nucleic acid amplification methods known in the art can be employed herein. As described above, when a nucleic acid amplification method is performed using a pair of polynucleotides for cancer detection as primers and a test nucleic acid as a template, the test nucleic acid is amplified. However, if no test nucleic acid is contained in a sample, amplification does not take place. Hence, through detection of amplification products, the presence or the absence of the test nucleic acid in a sample can be confirmed. An amplification product can be detected by a method that involves subjecting a reaction solution after amplification to electrophoresis, and then staining the band with ethidium bromide or the like or a method that involves immobilizing an amplification product after said electrophoresis onto a solid phase such as a nylon membrane, performing hybridization with a labeling probe that specifically hybridizes to a test nucleic acid, washing, and then detecting the label. Also, namely real-time detection PCR is performed using a quencher fluorescent dye and a reporter fluorescent dye, and thereby the amount of a test nucleic acid in a specimen can be quantitatively determined. Since kits for real-time detection PCR are commercially available, real-time detection PCR can be easily performed. Furthermore, semi-quantitative determination of a test nucleic acid is also possible based on electrophoresis band intensity. A test nucleic acid may be either mRNA or cDNA resulting from mRNA via reverse transcription. When mRNA is amplified as a test nucleic acid, a NASBA method (3SR method or TMA method) using the above primer pair can also be employed. The NASBA method itself is well-known and kits for the method are also commercially available, so that the method can be easily performed using the above primer pair.

[0063] As a probe, a labeled probe that is prepared by labeling a polynucleotide for cancer detection with a fluorescent label, a radiolabel, a biotin label, or the like can be used. A method for labeling a polynucleotide itself is well-known. The presence or the absence of a test nucleic acid in a sample can be examined by immobilizing a test nucleic acid or an amplification product thereof, performing hybridization with a labeled probe, washing, and then measuring the label bound to the solid phase. Alternatively, a polynucleotide for cancer detection is immobilized, a test nucleic acid is hybridized thereto, and then the test nucleic acid bound to the solid phase can be detected using the labeled probe or the like. In such a case, a polynucleotide for cancer detection bound to a solid phase is also referred to as a probe. A method for measuring a test nucleic acid using a polynucleotide probe is also known in the art. The method can be performed by causing, in a buffer, a polynucleotide probe to come into contact with a test nucleic acid at T_m or near T_m (preferably, within $\pm 4^\circ\text{C}$) for hybridization, washing, and then measuring the labeled probe that has hybridized or the template nucleic acid bound to the solid-phase probe. Examples of such method include well-known methods such as Northern blot, in situ hybridization, and Southern blot methods. In the present invention, any well-known method is applicable.

[0064] It is determined by the detection method of the present invention whether or not a subject animal has cancer based on the expression level of CAPRIN-1 measured as described above. Cancer can be detected only by measuring CAPRIN-1 expression in a subject animal. However, it is preferable in view of enhancing detection accuracy to examine the expression levels (antibody level, polypeptide level, or mRNA level) of CAPRIN-1 in one or a plurality of samples of healthy subjects so as to obtain a standard value of healthy subjects and then to compare the measured value of a subject animal with the standard value obtained from healthy subjects. To further enhance detection accuracy, CAPRIN-1 expression levels are examined for samples obtained from many patients found to have cancer so as to obtain a standard value of cancer patients and then the measured value of a subject animal may be compared with both the standard value of healthy subjects and the standard value of cancer patients. The above standard values can be determined by quantifying the CAPRIN-1 expression level in each sample and then calculating the mean value thereof, for example. A standard value of healthy subjects and the same of cancer patients can be determined in advance by examining CAPRIN-1 expression levels in many healthy subjects and cancer patients. Therefore, when comparison with a standard value is performed in the method of the present invention, a standard value determined in advance may be used.

[0065] In the detection method of the present invention, diagnosis based on other cancer antigens or cancer markers

may be used in combination. Accordingly, cancer detection accuracy can be further increased. For example, when an antibody specifically existing in cancer patients is measured by the method of the present invention, another polypeptide that is often expressed in a cancer tissue can be used in combination as an antigen in a manner similar to that for polypeptides above. Also, the method of the present invention and diagnosis using a previously known cancer marker may be performed in combination.

[0066] Cancer can be detected *in vivo* according to the detection method of the present invention. Particularly, as described in Examples below, even a small-size tumor, which is invisible to the naked eye, or a tumor in a deep part *in vivo* can be detected according to the method of the present invention. Thus, the method of the present invention is useful for early cancer detection. Also, through application of the detection method of the present invention for a patient during follow-up after treatment of cancer, cancer can be detected early if a cancer recurrence has taken place.

[0067] Also, in a cancer-bearing living organism, as the number of cancer cells expressing CAPRIN-1 measured in the present invention increases, the amounts of the protein and its mRNA accumulated in the living organism increase and the production amount of the antibody against CAPRIN-1 in serum increases. Meanwhile, as the number of cancer cells decreases, the amounts of the protein and its mRNA accumulated *in vivo* decrease and the amount of the antibody against CAPRIN-1 in serum decreases. Therefore, when the expression level of CAPRIN-1 is higher than that of a control, it can be determined that a tumor increase or a cancer metastasis is occurring; that is, the extent of cancer is advanced. Actually, as specifically described in the Examples below, an increase in the above serum antibody level in a cancer-bearing living organism was observed in association with cancer progression (malignant) such as tumor increase and metastasis. As described above, the extent of cancer can also be detected by the method of the present invention.

[0068] Also, as described in Examples below, among tumors of the same type, the above antibody levels in malignant type tumors were significantly higher than those in benign type tumors. Accordingly, when the expression level of CAPRIN-1 is high, it can be determined that cancer malignancy is higher. Specifically, cancer malignancy can also be detected by the method of the present invention.

[0069] Cancer to be subjected to the method for detecting cancer of the present invention is cancer expressing CAPRIN-1. Examples of such cancer include, but are not limited to, brain tumor, squamous cell carcinoma of the head, neck, lung, uterus or esophagus, melanoma, adenocarcinoma of the lung or uterus, renal cancer, malignant mixed tumor, hepatocellular carcinoma, basal cell carcinoma, acanthoma-like gingival tumor, tumor of the oral cavity, perianal adenocarcinoma, anal sac tumor, anal sac apocrine adenocarcinoma, sertoli cell carcinoma, cancer of the vaginal vestibule, sebaceous adenocarcinoma, sebaceous epithelioma, sebaceous adenoma, sweat gland carcinoma, intranasal adenocarcinoma, nasal adenocarcinoma, thyroid cancer, large-bowel cancer, bronchial adenocarcinoma, adenocarcinoma, ductal carcinoma, breast adenocarcinoma, composite type breast adenocarcinoma, malignant mammary mixed tumor, intraductal papillary adenocarcinoma, fibrosarcoma, hemangiopericytoma, osteosarcoma, chondrosarcoma, soft tissue sarcoma, histiocytic sarcoma, myxosarcoma, undifferentiated sarcoma, lung cancer, mastocytoma, cutaneous leiomyoma, intraperitoneal leiomyoma, leiomyoma, chronic lymphocytic leukemia, lymphoma, gastrointestinal lymphoma, digestive lymphoma, small-cell-to-medium-cell lymphoma, adrenomedullary tumor, granulosa cell tumor, and pheochromocytoma. Also, a living organism to be subjected to the method of the present invention is a mammal and is preferably a human, a dog, or a cat.

[0070] Examples of a sample to be subjected to the method of the present invention include body fluids such as blood, serum, blood plasma, ascites, and pleural effusion, tissues, and cells. In particular, in the 1st method and the 2nd method above, serum, blood plasma, ascites, and pleural effusion can be preferably used and in the 3rd method above for measurement of mRNA, tissue samples and cell samples are preferable.

[0071] The above polypeptides to be used as antigens for immunoassay in the 1st method (that is, the canine CAPRIN-1 of SEQ ID NO: 2 and a homolog thereof, a specifically reactive partial polypeptide, a specifically reactive modified polypeptide, and a specifically reactive addition polypeptide) can be provided as reagents for cancer detection. The reagent may consist of only the above polypeptide or may contain various additives or the like, for example, useful for stabilization of the polypeptide. Also, the reagent can be provided in a form immobilized onto a solid phase such a plate or a membrane. Preferable examples of the polypeptide are as described above.

[0072] An antibody that undergoes an antigen-antibody reaction with CAPRIN-1 or an antigen-binding fragment thereof, which is used for immunoassay of CAPRIN-1 itself in the 2nd method, can also be provided as a reagent for cancer detection. The reagent for cancer detection in this case may also consist of only the above antibody or an antigen-binding fragment thereof or may contain various additives or the like useful for stabilization and the like of the antibody or an antigen-binding fragment thereof. Also, the antibody or an antigen-binding fragment thereof may be in a form binding to a metal such as manganese or iron. When such metal-bound antibody or antigen-binding fragment thereof is administered to the body of a living organism, the metal-bound antibody or antigen-binding fragment thereof is accumulated at an increased level at a site where the antigen protein is present at a higher level. Therefore, the metal is measured by MRI or the like, and thereby the presence of cancer cells producing the antigen protein can be detected.

[0073] Furthermore, the above polynucleotide for cancer detection to be used for mRNA measurement in the 3rd method can also be provided as a reagent for cancer detection. The reagent for cancer detection in this case may also

consist of only the polynucleotide or may contain various additives and the like useful for stabilization and the like of the polynucleotide. The polynucleotide for cancer detection contained in the reagent is preferably a primer or a probe. Conditions and preferable examples of the polynucleotide for cancer detection are as described above.

5 EXAMPLES

[0074] The present invention will be described in more detail with reference to the examples set forth below; however, the technical scope of the present invention is not limited to the examples.

10 Example 1: Obtainment of new cancer antigen protein by SEREX method

(1) Construction of cDNA library

[0075] Total RNA was extracted from a testis tissue of a healthy dog by an Acid guanidium-Phenol-Chloroform method and then a polyA RNA was purified using Oligotex-dT30 mRNA purification Kit (Takara Shuzo Co., Ltd.) according to protocols included with the kit.

[0076] A canine testis cDNA phage library was synthesized using the thus obtained mRNA (5 μ g). The cDNA phage library was constructed using a cDNA Synthesis Kit, a ZAP-cDNA Synthesis Kit, and a ZAP-cDNA GigapackIII Gold Cloning Kit (STRATAGENE) according to protocols included with the kits. The size of the thus constructed cDNA phage library was 7.73×10^5 pfu/ml.

(2) Screening of cDNA library using serum

[0077] Immunoscreening was performed using the above constructed canine testis cDNA phage library. Specifically, host *Escherichia coli* (XL1-Blue MRF') was infected with the phage on an NZY agarose plate ($\Phi 90 \times 15$ mm) so as to obtain 2210 clones. *E. coli* cells were cultured at 42°C for 3 to 4 hours to form plaques. The plate was covered with a nitrocellulose membrane (Hybond C Extra: GE Healthcare Bio-Science) impregnated with IPTG (isopropyl- β -D-thiogalactoside) at 37°C for 4 hours, so that the protein was induced, expressed, and then transferred to the membrane. Subsequently, the membrane was collected and then immersed in TBS (10 mM Tris-HCl, 150 mM NaCl, and pH 7.5) containing 0.5% powdered skim milk, followed by overnight shaking at 4°C, thereby suppressing nonspecific reaction. The filter was reacted with a 500-fold diluted serum of a canine patient at room temperature for 2 to 3 hours.

[0078] As the above serum of a canine patient, a serum collected from a canine patient with breast cancer was used. These sera were stored at -80°C and then subjected to pre-treatment immediately before use. A method for pretreatment of serum is as follows. Specifically, host *Escherichia coli* (XL1-Blue MRF') was infected with a λ ZAP Express phage in which no foreign gene had been inserted and then cultured overnight on a NZY plate medium at 37°C. Subsequently, buffer (0.2 M NaHCO₃ and pH 8.3) containing 0.5 M NaCl was added to the plate, the plate was left to stand at 4°C for 15 hours, and then a supernatant was collected as an *Escherichia coli*/phage extract. Next, the thus collected *Escherichia coli*/phage extract was applied to an NHS-column (GE Healthcare Bio-Science), so that an *Escherichia coli*/phage-derived protein was immobilized. The serum of a canine patient was applied to the protein-immobilized column for reaction and then *Escherichia coli* and an antibody adsorbed to the phage were removed from the serum. The serum fraction that had passed through the column was diluted 500-fold with TBS containing 0.5% powdered skim milk. The resultant was used as an immunoscreening material.

[0079] A membrane onto which the treated serum and the above fusion protein had been blotted was washed 4 times with TBS-T (0.05% Tween20/TBS) and then caused to react with goat anti-canine IgG (Goat anti-Dog IgG-h+I HRP conjugated (BETHYL Laboratories)) diluted 5000-fold with TBS containing 0.5% powdered skim milk as a secondary antibody for 1 hour at room temperature. Detection was performed via an enzyme coloring reaction using an NBT/BCIP reaction solution (Roche). Colonies that matched sites positive for a coloring reaction were collected from the NZY agarose plate ($\Phi 90 \times 15$ mm) and then suspended in 500 μ l of an SM buffer (100 mM NaCl, 10 mM MgClSO₄, 50 mM Tris-HCl, 0.01% gelatin, and pH 7.5). Until colonies positive for coloring reaction were unified, secondary screening and tertiary screening were repeated by a method similar to the above, so that 30,940 phage clones reacting with serum IgG were screened. Thus, 5 positive clones were isolated.

(3) Homology search for isolated antigen gene

[0080] For nucleotide sequence analysis of the 5 positive clones isolated by the above method, a procedure for conversion from phage vectors to plasmid vectors was performed. Specifically, 200 μ l of a solution was prepared to contain host *Escherichia coli* (XL1-Blue MRF') so that absorbance OD₆₀₀ was 1.0. The solution was mixed with 250 μ l of a purified phage solution and then with 1 μ l of an ExAssist helper phage (STRATAGENE), followed by 15 minutes of

reaction at 37°C. Three milliliters of LB medium was added and then culture was performed at 37°C for 2.5 to 3 hours. Immediately after culture, the temperature of the solution was kept at 70°C by water bath for 20 minutes, centrifugation was performed at 4°C and 1000 × g for 15 minutes, and then the supernatant was collected as a phagemid solution. Subsequently, 200 µl of a solution was prepared to contain phagemid host *Escherichia coli* (SOLR) so that absorbance

OD₆₀₀ was 1.0. The solution was mixed with 10 µl of a purified phage solution, followed by 15 minutes of reaction at 37°C. The solution (50 µl) was seeded on LB agar medium containing ampicillin (to a final concentration of 50 µg/ml) and then cultured overnight at 37°C. Transformed SOLR single colonies were collected and then cultured in LB medium containing ampicillin (final concentration: 50 µg/ml) at 37°C. A plasmid DNA containing an insert of interest was purified using a QIAGEN plasmid Miniprep Kit (QIAGEN).

[0081] The purified plasmid was subjected to analysis of the full-length sequence by a primer walking method using the T3 primer according to SEQ ID NO: 31 and the T7 primer according to SEQ ID NO: 32. As a result of sequence analysis, the gene sequences according to SEQ ID NOS: 5, 7, 9, 11, and 13 were obtained. A homology search program, BLAST search (<http://www.ncbi.nlm.nih.gov/BLAST/>), was performed using the nucleotide sequences of the genes and amino acid sequences (SEQ ID NOS: 6, 8, 10, 12, and 14) of the proteins encoded by the genes. As a result of this homology search with known genes, it was revealed that all of the 5 obtained genes encoded CAPRIN-1. Regarding regions to be translated to proteins, the sequence identity among the 5 genes was 100% in terms of nucleotide sequence and 99% in terms of amino acid sequence. Also, regarding regions to be translated to proteins, the sequence identity between the genes and genes encoding human homolog thereof was 94% in terms of nucleotide sequence and 98% in terms of amino acid sequence. The nucleotide sequences of the human homolog are shown in SEQ ID NOS: 1 and 3 and the amino acid sequences of the same are shown in SEQ ID NOS: 2 and 4. Also, regarding regions to be translated to proteins, the sequence identity between the obtained canine genes and a gene encoding a cattle homolog was 94% in terms of nucleotide sequence and 97% in terms of amino acid sequence. The nucleotide sequence of the cattle homolog is shown in SEQ ID NO: 15 and the amino acid sequence of the same is shown in SEQ ID NO: 16. Regarding regions to be translated to proteins, the sequence identity between the genes encoding the human homolog and the gene encoding the cattle homolog was 94% in terms of nucleotide sequence and ranged from 93% to 97% in terms of amino acid sequence. Also, regarding regions to be translated to proteins, the sequence identity between the obtained canine genes and a gene encoding an equine homolog was 93% in terms of nucleotide sequence and 97% in terms of amino acid sequence. The nucleotide sequence of the equine homolog is shown in SEQ ID NO: 17 and the amino acid sequence of the same is shown in SEQ ID NO: 18. Regarding regions to be translated to proteins, the sequence identity between the genes encoding the human homolog and the gene encoding the equine homolog was 93% in terms of nucleotide sequence and 96% in terms of amino acid sequence. Also, regarding regions to be translated to proteins, the sequence identity between the obtained canine genes and genes encoding mouse homolog ranged from 87% to 89% in terms of nucleotide sequence and ranged from 95% to 97% in terms of amino acid sequence. The nucleotide sequences of the mouse homolog are shown in SEQ ID NOS: 19, 21, 23, 25, and 27 and the amino acid sequences of the same are shown in SEQ ID NOS: 20, 22, 24, 26, and 28. Regarding regions to be translated to proteins, the sequence identity between the genes encoding the human homolog and the genes encoding the mouse homolog ranged from 89% to 91% in terms of nucleotide sequence and ranged from 95% to 96% in terms of amino acid sequence. Also, regarding regions to be translated to proteins, the sequence identity between the obtained canine genes and a gene encoding a chicken homolog was 82% in terms of nucleotide sequence and 87% in terms of amino acid sequence. The nucleotide sequence of the chicken homolog is shown in SEQ ID NO: 29 and the amino acid sequence of the same is shown in SEQ ID NO: 30. Regarding regions to be translated to proteins, the sequence identity between the genes encoding the human homolog and the gene encoding the chicken homolog ranged from 81% to 82% in terms of nucleotide sequence and was 86% in terms of amino acid sequence.

(4) Gene expression analysis in each tissue

[0082] Expression of the genes obtained by the above method in canine and human normal tissues and various cell lines was examined by an RT-PCR (Reverse Transcription-PCR) method. A reverse transcription reaction was performed as follows. Specifically, total RNA was extracted from each tissue (50 mg to 100 mg) and each cell line (5 to 10 × 10⁶ cells) using a TRIZOL reagent (Invitrogen Corporation) according to protocols included therewith. cDNA was synthesized using the total RNA and Superscript First-Strand Synthesis System for RT-PCR (Invitrogen Corporation) according to protocols included therewith. PCR was performed as follows using primers specific to the obtained genes (according to SEQ ID NOS: 33 and 34). Specifically, PCR was performed by preparing a reaction solution adjusted to a total amount of 25 µl through addition of each reagent and an included buffer (0.25 µl of a sample prepared by reverse transcription reaction, the above primers (2 µM each), dNTP (0.2 mM each), and 0.65 U of ExTaq polymerase (Takara-baio Co., Ltd.)) and then by reacting the solution through repeating 30 times a cycle of 94°C/30 seconds, 60°C/30 seconds, and 72°C/30 seconds using a Thermal Cycler (BIO RAD). The gene-specific primers mentioned above were used to amplify the region between nucleotide 206 and nucleotide 632 in the nucleotide sequence of SEQ ID NO: 5 (canine CAPRIN-

1 gene) and the region between nucleotide 698 and nucleotide 1124 in the nucleotide sequence of SEQ ID NO: 1 (human CAPRIN-1 gene). For control, GAPDH-specific primers (according to SEQ ID NOS: 35 and 36) were used at the same time. As a result, as shown in Fig. 1, strong expression was observed in testis in the case of healthy canine tissues, while expression was observed in canine breast cancer and adenocarcinoma tissues. Furthermore, expression of the human homolog of the obtained genes was also confirmed. As a result, similarly to the case of canine CAPRIN-1 genes, expression could be confirmed only in the testis in the case of normal tissues. However, in the case of cancer cells, expression was detected in many types of cancer cell line, such as cell lines of breast cancer, brain tumor, leukemia, lung cancer, and esophageal cancer. Expression was confirmed in a particularly large number of breast cancer cell lines. Based on the results, it was confirmed that CAPRIN-1 expression was not observed in normal tissues other than those of the testis, while CAPRIN-1 was expressed in many cancer cells and particularly in breast cancer cell lines.

[0083] In addition, in Fig. 1, Reference No. 1 along the longitudinal axis indicates the expression pattern of each of the above-identified genes and Reference No. 2 along the same indicates the expression pattern of the GAPDH gene for control.

(5) Immunohistochemical staining

(5)-1 CAPRIN-1 expression in normal mouse and canine tissues

[0084] Mice (Balb/c, female) and dogs (beagle dogs, female) were exsanguinated under ether anesthesia and ketamine/isoflurane anesthesia. After laparotomy, organs (stomach, liver, eyeball, thymus gland, muscle, bone marrow, uterus, small intestine, esophagus, heart, kidney, salivary gland, large intestine, mammary gland, brain, lung, skin, adrenal gland, ovary, pancreas, spleen, and bladder) were each transferred to a 10cm dish containing PBS. Each organ was cut open in PBS and then fixed by perfusion overnight with 0.1 M phosphate buffer (pH 7.4) containing 4% paraformaldehyde (PFA). The perfusate was discarded, the tissue surface of each organ was rinsed with PBS, and then a PBS solution containing 10% sucrose was added to a 50ml centrifugal tube. Each tissue was then placed in each tube and then shaken using a rotor at 4°C for 2 hours. Each solution was substituted with a PBS solution containing 20% sucrose and then left to stand at 4°C until tissues precipitated. Each solution was substituted with a PBS solution containing 30% sucrose and then left to stand at 4°C until tissues precipitated. Each tissue was removed and a necessary portion was excised with a surgical scalpel. Next, an OCT compound (Tissue Tek) was applied and spread over each tissue surface, and then the tissues were placed on Cryomold. Cryomold was placed on dry ice for rapid freezing. Tissues were sliced into pieces 10 to 20 μ m long using a cryostat (LEICA) and then the sliced tissue pieces were air-dried on glass slides for 30 minutes using a hair dryer, so that glass slides onto which sliced tissue pieces had been applied were prepared. Next, each glass slide was placed in a staining bottle filled with PBS-T (saline containing 0.05% Tween20), so that a procedure involving exchange with PBS-T every 5 minutes was performed 3 instances. Excess water around each specimen was removed using Kimwipes and then each section was encircled using DAKOPEN (DAKO). As blocking solutions, a MOM mouse Ig blocking reagent (VECTASTAIN) was applied onto mouse tissue and PBS-T solution containing a 10% fetal calf serum was applied onto canine tissue. The resultants were left to stand in a moist chamber at room temperature for 1 hour. Next, a solution prepared with the blocking solution to a 10 μ g/ml anti-CAPRIN-1 monoclonal antibody (monoclonal antibody #8) having the heavy chain variable region of SEQ ID NO: 55 and the light chain variable region of SEQ ID NO: 56, which reacts with the cancer cell surfaces prepared in Example 3, was applied onto each slide glass and then left to stand within a moist chamber at 4°C overnight. After 3 instances of 10 minutes of washing with PBS-T, a MOM biotin-labeled anti-IgG antibody (VECTASTAIN) diluted 250-fold with the blocking solution was applied onto each glass slide and then left to stand within a moist chamber at room temperature for 1 hour. After 3 instances of 10 minutes of washing with PBS-T, an avidin-biotin ABC reagent (VECTASTAIN) was applied and then left to stand within a moist chamber at room temperature for 5 minutes. After 3 instances of 10 minutes of washing with PBS-T, a DAB staining solution (DAB 10 mg + 30% H_2O_2 10 μ l/0.05 M Tris-HCl (pH 7.6) 50 ml) was applied and then the glass slides were left to stand within a moist chamber at room temperature for 30 minutes. Glass slides were rinsed with distilled water and then a hematoxylin reagent (DAKO) was applied. After being left to stand at room temperature for 1 minute, the glass slides were rinsed with distilled water. The glass slides were immersed in 70%, 80%, 90%, 95%, and 100% ethanol solutions in such order for 1 minute each and then left to stand in xylene overnight. The glass slides were removed, coverslipped with Glycergel Mounting Medium (DAKO), and then observed. As a result, CAPRIN-1 expression was observed to a slight degree within cells in all salivary gland, kidney, colon, and stomach tissues, but CAPRIN-1 expression was never observed on cell surfaces. Also, absolutely no CAPRIN-1 expression was observed in tissues from other organs.

(5)-2 CAPRIN-1 expression in canine breast cancer tissue

[0085] With the use of 108 frozen canine breast cancer tissue specimens from dogs diagnosed by pathological diagnosis

as having malignant breast cancer, frozen section slides were prepared by a method similar to the above and immunohistochemical staining was performed using the monoclonal antibody #8 prepared in Example 3. As a result, CAPRIN-1 expression was confirmed in 100 out of the 108 specimens (92.5%). CAPRIN-1 was particularly strongly expressed on the surfaces of highly atypical cancer cells.

(5)-3 CAPRIN-1 expression in human breast cancer tissue

[0086] Immunohistochemical staining was performed using 188 breast cancer tissue specimens of a paraffin-embedded human breast cancer tissue array (BIOMAX). After 3 hours of treatment at 60°C, the human breast cancer tissue array was immersed into a staining bottle filled with xylene and then xylene replacement every 5 minutes was performed 3 instances. Next, a similar procedure was performed using ethanol and PBS-T instead of xylene. The human breast cancer tissue array was immersed into a staining bottle filled with 10 mM citrate buffer (pH6.0) containing 0.05% Tween20, treated for 5 minutes at 125°C, and then left to stand at room temperature for 40 minutes or more. Excess water around each specimen was removed from the array using Kimwipes, each section was encircled using DAKOPEN (DAKO), and then an appropriate amount of Peroxidase Block (DAKO) was added dropwise onto the array. The array was left to stand at room temperature for 5 minutes and then immersed into a staining bottle filled with PBS-T. PBS-T replacement every 5 minutes was performed 3 instances. As a blocking solution, a PBS-T solution containing 10% FBS was applied onto the array and then the array was left to stand within a moist chamber at room temperature for 1 hour. Next, the monoclonal antibody #8 prepared in Example 3 adjusted to 10 µg/ml using a PBS-T solution containing 5% FBS was applied and then the array was left to stand overnight within a moist chamber at 4°C. After 3 instances of 10 minutes of washing with PBS-T, an appropriate amount of Peroxidase Labeled Polymer Conjugated (DAKO) was added dropwise onto the array, and then the array was left to stand at room temperature for 30 minutes within a moist chamber. After 3 instances of 10 minutes of washing with PBS-T, a DAB staining solution (DAKO) was applied onto the array and then the array was left to stand at room temperature for 10 minutes. The DAB staining solution was discarded from the array and then 10 minutes of washing was performed with PBS-T for 3 instances. The array was rinsed with distilled water and then immersed in 70%, 80%, 90%, 95%, and 100% ethanol solutions in order for 1 minute each and then left to stand in xylene overnight. The array was removed, coverslipped with Glycergel Mounting Medium (DAKO), and then observed. As a result, strong CAPRIN-1 expression was observed for 138 (73%) out of the total 188 breast cancer tissue specimens. (5)-4 CAPRIN-1 expression in human malignant brain tumor

[0087] With the use of 247 malignant brain tumor tissue specimens of paraffin-embedded human malignant brain tumor tissue arrays (BIOMAX), immunohistochemical staining was performed by a method similar to that in (5)-3 above using the monoclonal antibody #8 prepared in Example 3. As a result, strong CAPRI-1 expression was observed in 227 (92%) out of the total 247 malignant brain tumor tissue specimens.

(5)-5 CAPRIN-1 expression in human breast cancer metastatic lymph node

[0088] With the use of 150 tissue specimens of human breast cancer metastatic lymph nodes of paraffin-embedded human breast cancer metastatic lymph node tissue arrays (BIOMAX), immunohistochemical staining was performed by a method similar to that in (5)-3 above using the monoclonal antibody #8 prepared in Example 3. As a result, strong CAPRIN-1 expression was observed in 136 (90%) out of the total 150 tissue specimens of human breast cancer metastatic lymph nodes. Specifically, it was revealed that CAPRIN-1 is also strongly expressed in a cancer tissue that has metastasized from breast cancer.

Example 2: Preparation of new canine and human cancer antigen proteins

(1) Preparation of recombinant protein

[0089] A recombinant protein was prepared by the following method based on the gene of SEQ ID NO: 5 obtained in Example 1. PCR was performed by preparing a reaction solution adjusted to a total amount of 50 µl through addition of each reagent and an included buffer (1 µl of a vector prepared from the phagemid solution obtained in Example 1 and then subjected to sequence analysis, 2 types of primer (0.4 µM each; according to SEQ ID NOS: 37 and 38) containing *Nde* I and *Kpn* I restriction enzyme cleavage sequences, 0.2 mM dNTP, 1.25 U PrimeSTAR HS polymerase (Takara-baio Co., Ltd.)) and then by reacting the solution through repeating 30 times a cycle of 98°C/10 seconds and 68°C/1.5 minutes using a Thermal Cycler (BIO RAD). The above 2 types of primer were used to amplify the region encoding the full-length amino acid sequence of SEQ ID NO: 6 (P47). After PCR, the thus amplified DNA was subjected to 1% agarose gel electrophoresis and then a DNA fragment of about 1.4 kbp was purified from the gel using a QIAquick Gel Extraction Kit (QIAGEN).

[0090] The purified DNA fragment was ligated to a pCR-Blunt cloning vector (Invitrogen Corporation). The vector was

transformed into *Escherichia coli* and then the plasmid was collected. It was confirmed based on the sequence that the amplified gene fragment matched the target sequence. The plasmid that matched the sequence of interest was treated with *Nde* I and *Kpn* I restriction enzymes and then the resultant was purified using a QIAquick Gel Extraction Kit. Then the gene sequence of interest was inserted into a pET30b expression vector (Novagen) for *Escherichia coli* treated with *Nde* I and *Kpn* I restriction enzymes. A His tag-fused recombinant protein can be produced using the vector. The plasmid was transformed into *Escherichia coli* BL21 (DE3) for expression and then expression induction was performed using 1 mM IPTG, so that the target protein was expressed within *Escherichia coli*.

[0091] Also, the recombinant protein of a canine homologous gene was prepared by the following method based on the gene of SEQ ID NO: 7. PCR was performed by preparing a reaction solution adjusted to a total amount of 50 μ l through addition of each reagent and an included buffer (1 μ l of cDNA from among cDNAs of various tissues and/or cells constructed in Example 1, for which the expression could be confirmed by an RT-PCR method, 2 types of primer (0.4 μ M each; according to SEQ ID NOS: 39 and 40) containing *Nde* I and *Kpn* I restriction enzyme cleavage sequences, 0.2 mM dNTP, 1.25 U PrimeSTAR HS polymerase (Takara-baio Co., Ltd.)) and then by reacting the solution through repeating 30 times a cycle of 98°C/10 seconds and 68°C/2.5 minutes using a Thermal Cycler (BIO RAD). The above 2 types of primer were used to amplify the region encoding the full-length amino acid sequence of SEQ ID NO: 8. After PCR, the thus amplified DNA was fractionated with 1% agarose gel electrophoresis and then a DNA fragment of about 2.2 kbp was purified using a QIAquick Gel Extraction Kit (QIAGEN).

[0092] The purified DNA fragment was ligated to pCR-Blunt cloning vector (Invitrogen Corporation). The vector was transformed into *Escherichia coli*, and then the plasmid was collected. It was then confirmed based on the sequence that the amplified gene fragment matched the sequence of interest. The plasmid that matched the sequence of interest was treated with *Nde* I and *Kpn* I restriction enzymes and then the resultant was purified using a QIAquick Gel Extraction Kit. Then the gene sequence of interest was inserted into a pET30b expression vector (Novagen) for *Escherichia coli* treated with *Nde* I and *Kpn* I restriction enzymes. A His tag-fused recombinant protein can be produced using the vector. The plasmid was transformed into *Escherichia coli* BL21 (DE3) for expression and then expression induction was performed using 1 mM IPTG, so that the protein of interest was expressed within *Escherichia coli*.

[0093] Also, the recombinant protein of a human homologous gene was prepared by the following method based on the gene of SEQ ID NO: 1. PCR was performed by preparing a reaction solution adjusted to a total amount of 50 μ l through addition of each reagent and an included buffer (cDNA (1 μ l) from among cDNAs of various tissues and/or cells constructed in Example 1, for which the expression could be confirmed by an RT-PCR method, 2 types of primer (0.4 μ M each; according to SEQ ID NOS: 41 and 42) containing *Sac* I and *Xho* I restriction enzyme cleavage sequences, 0.2 mM dNTP, 1.25 U PrimeSTAR HS polymerase (Takara-baio Co., Ltd.)) and then by reacting the solution through repeating 30 times a cycle of 98°C/10 seconds and 68°C/2.5 minutes using a Thermal Cycler (BIO RAD). The above 2 types of primer were used to amplify the region encoding the full-length amino acid sequence of SEQ ID NO: 2. After PCR, the thus amplified DNA was subjected to 1% agarose gel electrophoresis and then a DNA fragment of about 2.1 kbp was purified using a QIAquick Gel Extraction Kit (QIAGEN).

[0094] The purified DNA fragment was ligated to a cloning vector pCR-Blunt (Invitrogen Corporation). The vector was transformed into *Escherichia coli*, and then the plasmid was collected. It was then confirmed based on the sequence that the amplified gene fragment matched the sequence of interest. The plasmid that matched the sequence of interest was treated with *Sac* I and *Xho* I restriction enzymes and then the resultant was purified using a QIAquick Gel Extraction Kit. Then the gene sequence of interest was inserted into a pET30a expression vector (Novagen) for *Escherichia coli* treated with *Sac* I and *Xho* I restriction enzymes. A His tag-fused recombinant protein can be produced using the vector. The plasmid was transformed into *Escherichia coli* BL21 (DE3) for expression and then expression induction was performed using 1 mM IPTG, so that the protein of interest was expressed within *Escherichia coli*.

(2) Purification of recombinant protein

[0095] The above-obtained recombinant *Escherichia coli* expressing SEQ ID NO: 1, 5, or 7 was cultured at 37°C in LB medium containing 30 μ g/ml kanamycin until the absorbance at 600 nm reached around 0.7. Then isopropyl- β -D-1-thiogalactopyranoside was added to a final concentration of 1 mM, followed by 4 hours of culture at 37°C. Subsequently, cells were collected by 10 minutes of centrifugation at 4800 rpm. The cell pellet was suspended in phosphate buffered saline and then centrifuged at 4800 rpm for 10 minutes for washing cells.

[0096] The cells were suspended in phosphate buffered saline and then subjected to ultrasonication on ice. The thus ultrasonicated *Escherichia coli* solution was centrifuged at 6000 rpm for 20 minutes. The thus obtained supernatant was used as a soluble fraction and the thus obtained precipitate was used as an insoluble fraction.

[0097] The soluble fraction was added to a nickel chelate column (carrier: Chelating Sepharose (TradeMark) Fast Flow (GE Healthcare), column capacity: 5 mL, 50 mM hydrochloric acid buffer (pH 8.0) as equilibrated buffer) prepared according to a conventional method. The unbound fraction was washed with 50 mM hydrochloric acid buffer (pH 8.0) in an amount 10 times the capacity of the column and 20 mM phosphate buffer (pH 8.0) containing 20 mM imidazole.

Immediately after washing, 6 beds were eluted with 20 mM phosphate buffer (pH8.0) containing 100 mM imidazole. After the elution of the protein of interest had been confirmed by Coomassie staining, an elution fraction of 20 mM phosphate buffer (pH8.0) containing 100 mM imidazole was added to a strong anion exchange column (carrier: Q Sepharose (TradeMark) Fast Flow (GE Healthcare), column capacity: 5 mL, and 20 mM phosphate buffer (pH8.0) as equilibrated buffer). The unbound fraction was washed with 20 mM phosphate buffer (pH7.0) in an amount 10 times the column capacity and 20 mM phosphate buffer (pH7.0) containing 200 mM sodium chloride. Immediately after washing, 5 beds were eluted using 20 mM phosphate buffer (pH7.0) containing 400 mM sodium chloride. Thus, purified fractions of proteins each having the amino acid sequence shown in SEQ ID NO: 2, 6, or 8 were obtained. These purified fractions were then used as materials for an administration test. Fig. 2 shows the result of the protein of SEQ ID NO: 2 fractionated by electrophoresis and detected by Coomassie staining.

[0098] 200 μ l of each purified preparation obtained by the above method was dispensed into 1 ml of reaction buffer (20 mM Tris-HCl, 50 mM NaCl, 2 mM CaCl_2 pH7.4) and then 2 μ l of enterokinase (Novagen) was added. The preparation was left to stand at room temperature overnight for reaction, His tag was cleaved, and then purification was performed according to included protocols using an Enterokinase Cleavage Capture Kit (Novagen). Next, 1.2 ml of each purified preparation obtained by the above method was substituted with physiological phosphate buffer (Nissui Pharmaceutical Co., Ltd.) using ultrafiltration NANOSEP 10K OMEGA (PALL). Sterilized filtration was performed using 0.22 μ m HT Tuffryn Acrodisc (PALL) and then the resultants were used for the following experiments.

Example 3: Preparation of antibody against CAPRIN-1

(1) Preparation of polyclonal antibody against CAPRIN-1-derived peptide

[0099] To obtain an antibody binding to CAPRIN-1, CAPRIN-1-derived peptide (Arg-Asn-Leu-Glu-Lys-Lys-Lys-Gly-Lys-Leu-Asp-Asp-Tyr-Gln (SEQ ID NO: 43)) was synthesized. One milligram of the peptide as an antigen was mixed with an incomplete Freund's adjuvant (IFA) solution in an amount equivalent to the peptide. The mixture was subcutaneously administered to a rabbit 4 times every 2 weeks. Subsequently, blood was collected, so that an antiserum containing a polyclonal antibody was obtained. Furthermore, the antiserum was purified using a protein G carrier (GE Healthcare Bio-Sciences) and then a polyclonal antibody against the CAPRIN-1-derived peptide was obtained. Next, the reactivity of the obtained polyclonal antibody to the breast cancer cell surface was examined. Specifically, 10^6 cells of the MDA-MB-231 V human breast cancer cell line were subjected to centrifugation in a 1.5 ml microcentrifugal tube. A PBS solution supplemented with 0.1% fetal calf serum (FBS) containing the polyclonal antibody was added to the tube. The solution was left to stand on ice for 1 hour. After washing with PBS, an FITC-labeled goat anti-mouse IgG antibody (Invitrogen Corporation) diluted 500-fold with PBS containing 0.1% FBS was added to the solution, and then the solution was left to stand on ice for 1 hour. After washing with PBS, fluorescence intensity was measured using a FACS Calibur (Becton, Dickinson and Company). Meanwhile, a procedure similar to the above was performed so that a control was prepared by adding PBS containing 0.1% FBS instead of the polyclonal antibody. As a result, it was revealed that fluorescence intensity was found to be stronger in cells treated with the polyclonal antibody than that in control cells. Therefore, it was demonstrated that the obtained polyclonal antibody binds to the breast cancer cell surface.

(2) Preparation of monoclonal antibody against CAPRIN-1 protein

[0100] The antigen protein (human CAPRIN-1) (100 μ g) shown in SEQ ID NO: 2 prepared in Example 2 was mixed with a MPL+TDM adjuvant (Sigma) in an amount equivalent to that of the antigen protein. The mixture was used as an antigen solution per mouse. The antigen solution was administered intraperitoneally to a 6-week-old Balb/c mouse (Japan SLC Inc.) and then further administered 3 instances every week. Spleen was removed on day 3 after the final immunization and then ground in between two sterilized glass slides. The resultant was washed with PBS (-) (Nissui) and then centrifuged at 1500 rpm for 10 minutes, so that a procedure to remove supernatants was repeated 3 instances. Thus, spleen cells were obtained. The thus obtained spleen cells were mixed with mouse myeloma cells SP2/0 (purchased from ATCC) at a ratio of 10 : 1. The PEG solution prepared by mixing 200 μ l of RPMI1640 medium containing 10% FBS heated at 37°C and 800 μ l of PEG1500 (Boehringer) was added to the cells. The solution was left to stand for 5 minutes for cell fusion. Centrifugation was performed at 1700 rpm for 5 minutes to remove supernatants. Cells were suspended in 150 ml of RPMI1640 medium (HAT selective medium) containing 15% FBS, to which 2% equivalent of HAT solution (Gibco) had been added and then seeded onto fifteen 96-well plates (Nunc) at 100 μ l per well. Cells were cultured for 7 days under conditions of 37°C and 5% CO_2 , so that hybridomas resulting from fusion of spleen cells to myeloma cells were obtained.

[0101] Hybridomas were selected using as an index the binding affinity of the antibody produced by the thus prepared hybridomas for the CAPRIN-1 protein. The CAPRIN-1 protein solution (1 μ g/ml) prepared in Example 2 was added at 100 μ l per well of 96-well plates and then left to stand at 4°C for 18 hours. Each well was washed 3 instances with PBS-

T, and then 0.5% Bovine Serum Albumin (BSA) solution (Sigma) was added at 400 μ l per well, and then the plates were left to stand at room temperature for 3 hours. The solution was removed and then each well was washed 3 instances with 400 μ l of PBS-T. Each culture supernatant of the hybridomas obtained above was added at 100 μ l per well and then left to stand at room temperature for 2 hours. Each well was washed 3 instances with PBS-T, an HRP-labeled anti-mouse IgG (H+L) antibody (Invitrogen Corporation) diluted 5000-fold with PBS was added at 100 μ l per well and then left to stand at room temperature for 1 hour. Each well was washed 3 instances with PBS-T. A TMB substrate solution (Thermo) was added at 100 μ l per well and then left to stand for 15-30 minutes, so that a color reaction was performed. After color development, 1N sulfuric acid was added at 100 μ l per well to stop the reaction. Absorbance was measured at 450 nm and 595 nm using an absorption spectrometer. As a result, a plurality of hybridomas producing antibodies with high absorbances were selected.

[0102] The thus selected hybridomas were added at 0.5 hybridomas per well of 96-well plates and then cultured. After 1 week, hybridomas forming single colonies in wells were observed. Cells in these wells were further cultured. Hybridomas were selected using as an index the binding affinity of the antibody produced by cloned hybridomas for the CAPRIN-1 protein. The CAPRIN-1 protein solution (1 μ g/ml) prepared in Example 2 was added at 100 μ l per well of 96-well plates and then left to stand at 4°C for 18 hours. Each well was washed 3 instances with PBS-T. A 0.5% BSA solution was added at 400 μ l per well, and then left to stand at room temperature for 3 hours. The solution was removed and then each well was washed 3 instances with 400 μ l of PBS-T. Each culture supernatant of the hybridomas obtained above was added at 100 μ l per well and then left to stand at room temperature for 2 hours. Each well was washed 3 instances with PBS-T. An HRP-labeled anti-mouse IgG (H+L) antibody (Invitrogen Corporation) diluted 5000-fold with PBS was added at 100 μ l per well and then left to stand at room temperature for 1 hour. Each well was washed 3 instances with PBS-T, a TMB substrate solution (Thermo) was added at 100 μ l per well and then left to stand for 15-30 minutes, so that a color reaction was performed. After color development, 1N sulfuric acid was added at 100 μ l per well to stop the reaction. Absorbance was measured at 450 nm and 595 nm using an absorption spectrometer. As a result, a plurality of hybridoma cell lines producing monoclonal antibodies exerting reactivity to the CAPRIN-1 protein were obtained. Culture supernatants of hybridomas were purified using a protein G carrier, so that 150 monoclonal antibodies binding to the CAPRIN-1 protein were obtained.

[0103] Next, from among these monoclonal antibodies, monoclonal antibodies exerting reactivity to the surfaces of breast cancer cells expressing CAPRIN-1 were selected. Specifically, 10⁶ cells of the MDA-MB-231V human breast cancer cell line were subjected to centrifugation with a 1.5 ml microcentrifugal tube. The supernatant (100 μ l) of each hybridoma above was added and then left to stand on ice for 1 hour. After washing with PBS, an FITC-labeled goat anti-mouse IgG antibody (Invitrogen Corporation) diluted 500-fold with PBS containing 0.1 % fetal calf serum was added and then left to stand on ice for 1 hour. After washing with PBS, fluorescence intensity was measured using FACS Calibur (Becton, Dickinson and Company). Meanwhile, a procedure similar to the above was performed so that a control supplemented with a medium instead of the antibody was prepared. As a result, 10 monoclonal antibodies (# 1-# 10) having fluorescence intensity stronger than that of the control; that is, reacting with the surfaces of breast cancer cells were selected. The heavy chain variable regions and the light chain variable regions of these monoclonal antibodies were shown in SEQ ID NOS: 44-60. The above monoclonal antibody #1 comprises the heavy chain variable region of SEQ ID NO: 44 and the light chain variable region of SEQ ID NO: 45, the monoclonal antibody #2 comprises the heavy chain variable region of SEQ ID NO: 44 and the light chain variable region of SEQ ID NO: 46, the monoclonal antibody #3 comprises the heavy chain variable region of SEQ ID NO: 44 and the light chain variable region of SEQ ID NO: 47, the monoclonal antibody #4 comprises the heavy chain variable region of SEQ ID NO: 44 and the light chain variable region of SEQ ID NO: 48, the monoclonal antibody #5 comprises the heavy chain variable region of SEQ ID NO: 49 and the light chain variable region of SEQ ID NO: 50, the monoclonal antibody #6 comprises the heavy chain variable region of SEQ ID NO: 51 and the light chain variable region of SEQ ID NO: 52, the monoclonal antibody #7 comprises the heavy chain variable region of SEQ ID NO: 53 and the light chain variable region of SEQ ID NO: 54, the monoclonal antibody #8 comprises the heavy chain variable region of SEQ ID NO: 55 and the light chain variable region of SEQ ID NO: 56, the monoclonal antibody #9 comprises the heavy chain variable region of SEQ ID NO: 57 and the light chain variable region of SEQ ID NO: 58, and the monoclonal antibody #10 comprises the heavy chain variable region of SEQ ID NO: 59 and the light chain variable region of SEQ ID NO: 60.

(3) Identification of a peptide in CAPRIN-1 protein, to which an antibody against CAPRIN-1 reacting to cancer cell surface binds

[0104] With the use of monoclonal antibodies #1-#10 against CAPRIN-1, reacting with the surfaces of cancer cells obtained above, partial sequences in the CAPRIN-1 protein to be recognized by these monoclonal antibodies were identified.

[0105] First, DTT (Fluka) was added to 100 μ l of a recombinant CAPRIN-1 protein solution adjusted to contain the protein at a concentration of 1 μ g/ μ l with PBS to a final concentration of 10 mM, followed by 5 minutes of reaction at

95°C, so that reduction of disulfide bonds within the CAPRIN-1 protein was performed. Next, iodoacetamide (Wako Pure Chemical Industries, Ltd.) with a final concentration of 20 mM was added and then an alkylation reaction was performed for thiol groups at 37°C for 30 minutes under shading conditions. Fifty microgram each of monoclonal antibodies #1-#10 against CAPRIN-1 was added to 40 µg of the thus obtained reduced-alkylated CAPRIN-1 protein. The volume of the mixture was adjusted to 1 mL of 20 mM phosphate buffer (pH7.0), and then the mixture was left to react overnight at 4°C while stirring and mixing each mixture.

[0106] Next, trypsin (Promega) was added to a final concentration of 0.2 µg. After 1 hour, 2 hours, 4 hours, and then 12 hours of reaction at 37°C, the resultants were mixed with protein A-glass beads (GE) subjected in advance to blocking with PBS containing 1% BSA (Sigma) and washing with PBS in 1 mM calcium carbonate and NP-40 buffer (20 mM phosphate buffer (pH7.4), 5 mM EDTA, 150 mM NaCl, and 1% NP-40), followed by 30 minutes of reaction.

[0107] The reaction solutions were each washed with 25 mM ammonium carbonate buffer (pH8.0) and then antigen-antibody complexes were eluted using 100 µl of 0.1% formic acid. LC-MS analysis was conducted for eluates using Q-TOF Premier (Waters-MicroMass) according to protocols included with the instrument.

[0108] As a result, the polypeptide of SEQ ID NO: 61 was identified as a partial sequence of CAPRIN-1, which was recognized by all of the monoclonal antibodies #1-#10 against CAPRIN-1. Furthermore, the peptide of SEQ ID NO: 62 was identified as a partial sequence in the polypeptide of (SEQ ID NO: 61 above, which was recognized by the monoclonal antibodies #1-#4, #5-#7, and #9. It was further revealed that the monoclonal antibodies #1-#4 recognized the peptide of SEQ ID NO: 63 that was a partial sequence peptide thereof.

Example 4: Cancer diagnosis using CAPRIN-1 polypeptide

(1) Canine cancer diagnosis

[0109] Blood was collected from 342 canine patients confirmed to have malignant or benign tumors and 6 healthy dogs, and serum was separated. With the use of the canine CAPRIN-1 polypeptide (SEQ ID NO: 8) and the anti-canine IgG antibody prepared in Example 2, the titer of the serum IgG antibody specifically reacting with the polypeptide was measured by an ELISA method.

[0110] Immobilization of the thus prepared polypeptide was performed by adding a recombinant protein solution diluted to 5 µg/mL with phosphate buffered saline to 96-well immobilizer amino plates (Nunc) at 100 µl/well and then leaving the plates to stand at 4°C overnight. Blocking was performed by adding a 50 mM sodium bicarbonate buffer solution (pH 8.4) (hereinafter, blocking solution) containing 0.5% BSA (bovine serum albumin) (Sigma Aldrich Japan) at 100 µl/well and then shaking the solution at room temperature for 1 hour. Serum diluted 1000-fold with the blocking solution was added at 100 µl/well and then the mixture was shaken at room temperature for 3 hours for reaction. The reaction solutions were washed 3 instances with phosphate buffered saline (hereinafter, PBS-T) containing 0.05% Tween20 (Wako Pure Chemical Industries, Ltd.). An HRP modified canine IgG antibody (Goat anti-Dog IgG-h+I HRP conjugated: BETHYL Laboratories) diluted 3000-fold with the blocking solution was added at 100 µl/well, followed by 1 hour of reaction at room temperature while shaking the solution. After 3 instances of washing with PBS-T, HRP substrate TMB (1-Step Turbo TMB (tetramethylbenzidine), PIERCE) was added at 100 µl/well and then an enzyme-substrate reaction was conducted at room temperature for 30 minutes. Subsequently, a 0.5 M sulfuric acid solution (Sigma Aldrich Japan) was added at 100 µl/well to stop the reaction. Absorbance at 450 nm was measured using a microplate reader. As controls, a specimen in connection with which no recombinant protein prepared had been immobilized and a specimen in connection with which a reaction with the serum of a cancer-bearing dog had not been conducted were similarly subjected to the above treatment and comparison.

[0111] As a result of pathologic diagnosis using excised tumor tissue, definitive diagnosis was made indicating that 215 out of the total 342 specimens used for the cancer diagnosis were malignant.

[0112] Specifically, specimens were diagnosed as having cancer such as malignant melanoma, malignant mixed tumor, hepatocellular carcinoma, basal cell carcinoma, acanthoma-like gingival tumor, tumor of oral cavity, perianal adenocarcinoma, anal sac tumor, anal sac apocrine adenocarcinoma, Sertoli cell carcinoma, cancer of vaginal vestibule, sebaceous adenocarcinoma, sebaceous epithelioma, sebaceous adenoma, sweat gland carcinoma, intranasal adenocarcinoma, nasal adenocarcinoma, thyroid cancer, large-bowel cancer, bronchial adenocarcinoma, adenocarcinoma, ductal carcinoma, breast adenocarcinoma, composite type breast adenocarcinoma, malignant mammary mixed tumor, intraductal papillary adenocarcinoma, fibrosarcoma, hemangiopericytoma, osteosarcoma, chondrosarcoma, soft tissue sarcoma, histiocytic sarcoma, myxosarcoma, undifferentiated sarcoma, lung cancer, mastocytoma, cutaneous leiomyoma, intraperitoneal leiomyoma, leiomyoma, squamous cell carcinoma, chronic lymphocytic leukemia, lymphoma, gastrointestinal lymphoma, digestive lymphoma, small-cell-to-medium-cell lymphoma, adrenomedullary tumor, granulosa cell tumor, and pheochromocytoma.

[0113] The sera from the living bodies of these cancer-bearing dogs were found to have significantly high antibody titers against the recombinant protein as shown in Fig. 3. When the reference value as malignant cancer regarding the

diagnostic method was determined to be twice or more the average value for healthy dogs, it was demonstrated that malignancy could be diagnosed for 108 specimens, which accounted for accounting for 50.2% of all the specimens. The cancer types of these 108 specimens are as follows. Although development of a plurality of types of cancer had indicated for some specimens, the following numerical values are cumulative total values for each cancer type:

6 cases of malignant melanoma, 11 cases of lymphoma, 1 case of suppurative inflammation, 1 case of granulosa cell tumor, 4 cases of hepatocellular carcinoma, 3 cases of malignant testicular tumor, 3 cases of tumor of oral cavity, 7 cases of perianal adenocarcinoma, 12 cases of sarcoma, 35 cases of breast adenocarcinoma, 1 case of lung cancer, 6 cases of ductal carcinoma, 2 cases of sebaceous adenocarcinoma, 5 cases of mastocytoma, 1 case of smooth muscle sarcoma, 3 cases of squamous cell carcinoma, 2 cases of malignant mixed tumor, 1 case of hemangiopericytoma, 1 case of transitional epithelial cancer, 1 case of hemangiopericytoma, 1 case of hemangiopericytoma, and 1 case of sebaceous epithelioma.

[0114] As a result of similar diagnosis using pleural effusions and ascites collected from canine patients with terminal cancer, values similar to the results obtained by the diagnostic method using serum could be detected and cancer diagnosis could be made.

[0115] Also, it was demonstrated that the use of the diagnostic method enables diagnosis of cancer in a location invisible to the naked eye, the extent of cancer, malignancy or postoperative course of cancer, recurrence, metastasis, and the like. Several specific examples of detailed diagnosis shown in Fig. 4 are as described below.

(2)-1 Cancer diagnosis for tumor invisible to the naked eye

[0116] On June 7, 2007, no tumor mass was confirmed for canine patient 1 (flat coated retriever). However, about 20 days later, on June 24, 2007, a peduncular tumor mass with a diameter of 2 mm was found in the gum at the root of the maxillary left cuspid tooth of canine patient 1. On the day when the mass was found, the peduncular portion was ligated and excised. Absorbance at 450 nm was found to be 0.06 before the tumor mass could be visually confirmed, and this figure was almost the same as 0.04, which was determined when the tumor was found. It was also demonstrated by the result that diagnosis of cancer in a location invisible to the naked eye, such as intraperitoneal cancer, is possible with the use of this technique.

[0117] In addition, it can be said that a warning sign of tumor development was successfully detected, since a rise in the aforementioned level could be confirmed before the tumor could be confirmed with the naked eye. Hence, it was confirmed that the technique is also useful for health examinations such as routine health checkups.

(2)-2 Diagnosis of the extent of cancer

[0118] The extent of cancer is determined based on tumor size, tumor depth, how the tumor affects the peripheral tissue, and the presence or the absence of metastasis. It was revealed that a higher value was detected when metastasis had occurred or cancer had progressed.

(2)-3 Diagnosis of cancer malignancy

[0119] Basal cell tumors include malignant basal cell tumors and benign basal cell tumors. In recent year, malignant basal cell tumors have tended to be classified as examples of basal cell carcinoma and benign basal cell tumors tend to be classified as examples of trichoblastoma according to the new WHO.

[0120] Canine patient 2 (Beagle) diagnosed as having basal cell carcinoma (malignant) was subjected to serodiagnosis upon surgery, so that the absorbance at 450 nm was found to be 0.04. Meanwhile, canine patient 3 (mongrel) diagnosed as having trichoblastoma (benign) was subjected to serodiagnosis upon surgery, so that the absorbance at 450 nm was found to be 0, indicating no detection. Therefore, it was demonstrated that different types of basal cell tumor, i.e., malignant basal cell carcinoma and benign trichoblastoma, can be diagnosed, even if they are classified as basal cell tumors.

[0121] Next, examples of mammary gland tumors are as follows. Mammary gland tumors are classified as malignant tumors such as breast adenocarcinoma and malignant mammary mixed tumor and benign mammary gland tumors exhibiting no malignant findings.

[0122] Canine patient 4 (Shetland Sheepdog) underwent extirpative surgery on July 17, 2007, for breast adenocarcinoma. Canine patient 4 had 3 tumors. Pathologic diagnosis using isolated tissue resulted in the same diagnosis. Strongly atypical and invasive mammary gland tissue experienced somewhat widespread papillary-adenoid growth, and vascular invasion was also confirmed for the specimens. Thus, canine patient 4 was diagnosed as having highly malignant breast cancer. As a result of serodiagnosis using blood collected upon surgery, absorbance at 450 nm was found to be 0.41.

[0123] Meanwhile, canine patient 5 (toy poodle) had extirpative surgery on October 9, 2007, for a mammary gland tumor. Pathologic diagnosis using isolated tissues at this time revealed that: whereas tumors were formed in which mammary gland epithelial cells and myoepithelial cells grew, myoepithelial cell components were uniform spindle cells and no malignancy was detected; and the mammary gland epithelial cell component exhibited a slight difference in size and dyskaryosis as observed. Hence, canine patient 5 was diagnosed as having a benign mammary gland tumor for which no malignancy was detected. As a result of blood collection and serodiagnosis upon surgery thereof, absorbance at 450 nm was found to be 0.

[0124] The above results for the 2 specimens revealed that the malignancy of a highly malignant tumor is greater than that of a benign low-malignant tumor.

[0125] Also, distribution of the diagnoses for 54 malignant tumor (breast cancer) specimens, such as breast adenocarcinoma or malignant mammary mixed tumor specimens and 21 benign mammary gland tumor specimens exhibiting no malignancy, were examined. Whereas benign mammary gland tumor specimens showed a distribution similar to that in the case of healthy dogs, breast cancer specimens showed a distribution of high values.

(2)-4 Diagnosis of postoperative course

[0126] Canine patient 6 (mongrel) visited the hospital because of mastocytoma and had extirpative surgery on May 23, 2005. As a result of serodiagnosis made at this time, absorbance at 450 nm was found to be 0.10. Mastocytoma is a tumor that repeatedly undergoes recurrence or metastasis when resected incompletely. Hence, whether or not complete tumor resection can be achieved by surgery is important. At the follow-up on December 19, 2006, absorbance at 450 nm was found to be 0.05, so that a decreased antibody titer was confirmed. At this time, no recurrence was confirmed. Hence, in the case of canine patient 6, it can be said that since the tumor could be completely resected, the serodiagnosis results were lower than those upon surgery.

[0127] Canine patient 7 (Beagle) had extirpative surgery on February 14, 2008, for mastocytoma. As a result of serodiagnosis performed at this time, absorbance at 450 nm was found to be 0.17. As a result of histopathological diagnosis using excised tissues, invasive hyperplasia was observed and Canine patient 7 was diagnosed as having mastocytoma corresponding to the moderately differentiated type (Patnaik II type). Canine patient 7 visited again for follow-up on March 10, 2008 and was subjected to serodiagnosis again. As a result, absorbance at 450 nm was found to be 0.07. At this time, neither metastasis nor recurrence was confirmed. Thus, in the case of canine patient 7, it can be said that the serodiagnosis results were lower than those upon surgery since the tumor could be completely resected.

(2)-5 Recurrence diagnosis

[0128] Canine patient 8 (Husky) had extirpative surgery on May 8, 2007, for breast adenocarcinoma. As a result of serodiagnosis performed at this time, absorbance at 450 nm was found to be 0.05. As a result of pathologic diagnosis using excised tissue, strongly atypical epithelial cells grew mainly forming a tubular structure. Thus, canine patient 8 was diagnosed as having adenocarcinoma from the primary mammary gland. At this time, the presence of many cancer cells in lymph ducts had already been confirmed, indicating a high risk of metastasis to or recurrence at the lymph nodes or distant sites. On June 28, 2007, (about 1 and a half months after surgery), recurrence was confirmed at the same site. The result of serodiagnosis at this time was 0.09, and thus an increased value was confirmed. In the case of canine patient 8, it was revealed that because of incomplete tumor resection or recurrence thereof, the diagnostic results were higher in late June than in early May.

(2)-6 Diagnosis of metastasis

[0129] Canine patient 9 (Scottish terrier) experienced multiple metastases and recurrences, including a mammary gland tumor in February 2003, intraoral malignant melanoma in August 2003, labial malignant melanoma in January 2005, and intraoral melanoma on April 13, 2005. All of these tumors had been resected by surgery. Canine patient 9 revisited the hospital on December 17, 2006, for follow-up after the recurrence of intraoral melanoma on April 2005 and was subjected to serodiagnosis. As a result, absorbance at 450 nm was found to be 0.09. Half a year later, canine patient 9 revisited the hospital on June 20, 2007 because of cervical lymphoid and popliteal lymphoid hyperplasia. In the case of lymphoma, the lymph nodes swell up systemically. Canine patient 9 had swelling lymph nodes at only two sites. Hence, canine patient 9 was clinically diagnosed as likely to have lymphoma due to metastasis. Diagnosis made by this technique also revealed that absorbance at 450 nm was increased to 0.10, indicating that the lymphoma was caused by metastasis from the previous tumor.

[0130] Canine patient 10 (Shiba inu) underwent tumorectomy on March 11, 2006, because of intraoral malignant melanoma of the right lip. Canine patient 10 had a history of treatment with an anticancer agent (cyclophosphamide) from June 10, 2006, to September 26, 2006, and had been under medication with BIREMO S having organic germanium

as a major ingredient since May 23, 2006. Serodiagnosis was made on March 20, 2007, upon the removal of a tumor thought to have resulted from metastasis of the previous tumor, so that the absorbance at 450 nm was found to be almost 0.03, indicating almost no detection. Pathologic diagnosis was made for the tissue excised at this time so that the disease was diagnosed as metastatic malignant melanoma. However, metastasis occurred again on June 27, 2007, 3 months after surgery for metastatic melanoma. A tumor developed at the right portion of the cervix on March 20, 2007, and further tumor development occurred on the side opposite to such portion on June 27, 2007. The tumors formed black masses analogous to those of the previous findings. Tumor size was 3.1 x 3.2 x 0.8 cm, and the tumors were clinically diagnosed as metastatic tumors. As a result of serodiagnosis at this time, absorbance at 450 nm was confirmed to have increased to 0.23, suggesting that the tumors resulted from metastasis of previous tumors.

(2)-7 Cancer diagnosis using human CAPRIN-1-derived polypeptide

[0131] With the use of the polypeptide (SEQ ID NO: 2) of human CAPRIN-1 prepared in Example 2, the titer of canine serum IgG antibody reacting with the polypeptide was measured in a manner similar to that used above. As a result of examination using serum of a healthy dog, almost no absorbance was detected at 450 nm, similarly to the case above.

[0132] Meanwhile, canine patient 11 (Shih tzu) had extirpative surgery for breast adenocarcinoma on June 21, 2007. As a result of pathologic diagnosis using excised tissues, canine patient 11 was diagnosed as having breast adenocarcinoma of moderate malignancy, wherein strongly atypical and invasive mammary gland tissues underwent adenoid-tubular-papillary growth so as to form large and small masses, in addition to the presence of somewhat diffuse hyperplasia of fibrillar connective tissues. The absorbance at 450 nm for canine patient 11 was found to be 0.26.

(3) Feline cancer diagnosis

[0133] Next, cancer-bearing cats and healthy cats were diagnosed. With the use of the polypeptide of canine CAPRIN-1 (used above) and an anti-feline IgG antibody, the titer of feline serum IgG antibody specifically reacting with the polypeptide was measured, in a manner similar to the above. As a secondary antibody, an HRP modified anti-feline IgG antibody (PEROXIDASE-CONJUGATED GOAT IgG FRACTION TO CAT IgG (WHOLE MOLECULE): CAPPEL RESEARCH REAGENTS) was diluted 8000-fold with a blocking solution and then used.

[0134] Feline patient 1 (mongrel) had tumor extirpative surgery for breast adenocarcinoma on May 8, 2007. The absorbance at 450 nm for feline patient 1 was found to be 0.21. Also, in the case of feline patient 2 (Himalayans) that had extirpative surgery for ductal carcinoma on October 17, 2006, the absorbance at 450 nm was found to be 0.18. On the other hand, no absorbance was detected in the case of healthy cats.

[0135] Also, with the use of the polypeptide (SEQ ID NO: 2) of human CAPRIN-1 prepared in Example 2, the titer of feline serum IgG antibody reacting with the polypeptide was measured in a manner similar to the above. As a result, in the case of healthy cats, almost no absorbance was detected at 450 nm when the polypeptide had been immobilized. Meanwhile, feline patient 3 (American Shorthair) had extirpative surgery for breast adenocarcinoma on April 15, 2008. As a result of pathologic diagnosis using excised tissues, feline patient 3 was diagnosed as having highly malignant breast adenocarcinoma associated with large and small dead tissues, wherein strongly atypical and invasive mammary gland tissues underwent sheet-like growth into large and small masses. Also in the case of feline patient 3, the absorbance at 450 nm was found to be 0.12.

[0136] Therefore, it was demonstrated that cancer diagnosis is also possible for cats by this technique, similarly to dogs, since values were detected for specimens from cats with cancer, but none was detected for specimens from healthy cats.

(4) Human cancer diagnosis

[0137] With the use of the polypeptide (SEQ ID NO: 2) of human CAPRIN-1 prepared in Example 2 and an anti-human IgG antibody, the titer of a healthy human serum IgG antibody specifically reacting with the polypeptide was measured. Immobilization of the prepared polypeptide was performed by adding a recombinant protein solution diluted to 100 µg/mL with phosphate buffered saline to 96-well immobilizer amino plates (Nunc) at 100 µl/well and then leaving the plates to stand overnight at 4°C. Blocking was performed as follows. Four gram of Block Ace powder (DS PHARMA BIOMEDICAL Co., Ltd.) was dissolved in 100 ml of purified water and then the solution was diluted 4-fold with purified water. Then the solution (hereinafter, blocking solution) was added at 100 µl/well and then shaken at room temperature for 1 hour. Serum diluted 1000-fold with the blocking solution was added at 100 µl/well and then shaken at room temperature for 3 hours for reaction. After washing 3 instances with phosphate buffered saline (hereinafter, PBS-T) containing 0.05% Tween20 (Wako Pure Chemical Industries, Ltd.), an HRP-modified anti-human IgG antibody (HRP-Goat Anti-Human IgG (H+L) Conjugate: Zymed Laboratories) diluted 10000-fold with the blocking solution was added at 100 µl/well and then shaken at room temperature for 1 hour for reaction. After 3 instances of washing with PBS-T, HRP substrate TMB (1-Step Turbo

TMB (tetramethylbenzidine, PIERCE) was added at 100 μ l/well and then an enzyme-substrate reaction was performed at room temperature for 30 minutes. Subsequently, a 0.5 M sulfuric acid solution (Sigma Aldrich Japan) was added at 100 μ l/well to stop the reaction and then absorbance at 450 nm was measured using a microplate reader. An ovalbumin antigen adjusted to 50 μ g/ml with phosphate buffered saline was immobilized and then used as a positive control. As a result, absorbance at 450 nm was found to be as high as 0.45 on average as the results for 7 healthy subjects in the case of the ovalbumin antigen, but no absorbance (0) was detected in the case of the above polypeptide.

[0138] In a manner similar to the above, 17 serum specimens (purchased from ProMedDx) from patients with malignant breast cancer were further subjected to measurement of the titer of serum IgG antibody specifically reacting with the human-derived cancer antigen protein (the amino acid sequence of SEQ ID NO: 3). As a result, absorbance at 450 nm was found to be as high as 0.48 in the case of the above polypeptide, on average as the results for 17 breast cancer patients.

[0139] Also, with the use of the polypeptide (SEQ ID NO: 8) of canine CAPRIN-1 prepared in Example 2 and an anti-human IgG antibody, the titer of human serum IgG antibody specifically reacting with the polypeptide was measured in a manner similar to that above. As a result, whereas the average of the results for 7 healthy subjects was 0.04, the average of the results for 17 breast cancer patients was as high as 0.55.

[0140] Based on the above results, it was demonstrated that cancer in humans can also be detected by this technique.

Example 5: Cancer diagnosis through measurement of antigen polypeptide

[0141] With the use of the polyclonal antibody against CAPRIN-1-derived peptide (SEQ ID NO: 43) obtained in Example 3 (1) and each monoclonal antibody against the CAPRIN-1 protein obtained in Example 3 (2) in combination, the antigen polypeptide itself contained in specimens (cancer-bearing living organism-derived serum) reacted positive upon cancer diagnosis using the polypeptide of CAPRIN-1 in Example 4 (1)-(3) was detected by Sandwich ELISA. The polyclonal antibody was used as a primary antibody and each monoclonal antibody was used as a secondary antibody. The serum protein level of the protein specifically reacting with each of the above antibodies was measured.

[0142] The primary antibody was immobilized by adding the polyclonal antibody diluted to a concentration of 5 μ g/ml with phosphate buffered saline to 96-well immobilizer amino plates (Nunc) at 100 μ l/well and then shaking the plates at room temperature for 2 hours. Blocking was performed by adding a 50 mM sodium bicarbonate buffer solution (pH 8.4) (hereinafter, blocking solution) containing 0.5% BSA (bovine serum albumin, Sigma Aldrich Japan) at 100 μ l/well and then shaking at room temperature for 1 hour. Subsequently, a cancer-bearing living organism-derived serum diluted using the blocking solution was added at 100 μ l/well and then the resultants were shaken at room temperature for 3 hours for reaction. The dilution rate at this time was adjusted with 10-fold (10-1000-fold) dilution series. After 3 instances of washing with phosphate buffered saline (hereinafter, PBS-T) containing 0.05% Tween20 (Wako Pure Chemical Industries, Ltd.), each monoclonal antibody as a secondary antibody diluted to a concentration of 1 μ g/ml with the blocking solution was added at 100 μ l/well and then the resultants were shaken at room temperature for 1 hour for reaction. After 3 instances of washing with PBS-T, an HRP-labeled anti-mouse IgG (H+L) antibody (Invitrogen Corporation) as a tertiary antibody diluted 5000-fold with the blocking solution was added at 100 μ l per well and then left to stand at room temperature for 1 hour. After 3 instances of washing of wells with PBS-T, a TMB substrate solution (Thermo) was added at 100 μ l per well and then left to stand for 15-30 minutes for color reaction. After color development, 1 N sulfuric acid was added at 100 μ l per well to stop the reaction and then absorbance at 450 nm was measured using an absorption spectrometer.

[0143] As a result, when the #1-#10 monoclonal antibodies reacting with the surfaces of cancer cells were used as secondary antibodies, absorbance values (polypeptide levels) of 0.3 or higher were detected for all specimens from cancer-bearing dogs and cancer-bearing cats with breast cancer, malignant melanoma, and the like, but no absorbance was detected for healthy dogs and healthy cats. On the other hand, when monoclonal antibodies reacting with the CAPRIN-1 protein itself but not reacting with the surfaces of cancer cells were used as secondary antibodies, polypeptide levels were detected for all specimens, but absorbance values were all 0.05 or less, which were lower than the results for combinations of antibodies reacting with the surfaces of cancer cells.

[0144] Therefore, cancer can also be diagnosed by this technique that involves detection of antigen polypeptides using antibodies against CAPRIN-1.

INDUSTRIAL APPLICABILITY

[0145] The present invention is industrially useful for diagnosis or detection of cancer.

[0146] This description includes part or all of the contents as disclosed in the description and/or drawings of Japanese Patent Application No. 2008-202320, which is a priority document of the present application. Also, all publications, patents, and patent applications cited herein are incorporated herein by reference in their entirety.

SEQUENCE LISTING FREE TEXT

SEQ ID NOS: 31-42: primers

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40	Arg Leu Lys Thr Val Leu Glu Leu Gln Tyr Val Leu Asp Lys Leu Gly		
		145	150 155 160
45	Asp Asp Glu Val Arg Thr Asp Leu Lys Gln Gly Leu Asn Gly Val Pro		
		165	170 175
50	Ile Leu Ser Glu Glu Glu Leu Ser Leu Leu Asp Glu Phe Tyr Lys Leu		
		180	185 190

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Val Asp Pro Glu Arg Asp Met Ser Leu Arg Leu Asn Glu Gln Tyr Glu
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His Ala Ser Ile His Leu Trp Asp Leu Leu Glu Gly Lys Glu Lys Pro
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Val Cys Gly Thr Thr Tyr Lys Val Leu Lys Glu Ile Val Glu Arg Val
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Phe Gln Ser Asn Tyr Phe Asp Ser Thr His Asn His Gln Asn Gly Leu
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Cys Glu Glu Glu Glu Ala Ala Ser Ala Pro Ala Val Glu Asp Gln Val
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Pro Glu Ala Glu Pro Glu Pro Ala Glu Glu Tyr Thr Glu Gln Ser Glu
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Val Glu Ser Thr Glu Tyr Val Asn Arg Gln Phe Met Ala Glu Thr Gln
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Phe Thr Ser Gly Glu Lys Glu Gln Val Asp Glu Trp Thr Val Glu Thr
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Val Glu Val Val Asn Ser Leu Gln Gln Gln Pro Gln Ala Ala Ser Pro
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Ser Val Pro Glu Pro His Ser Leu Thr Pro Val Ala Gln Ala Asp Pro
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Leu Val Arg Arg Gln Arg Val Gln Asp Leu Met Ala Gln Met Gln Gly

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10	Leu Asp Pro Ala Ile Val Ser Ala Gln Pro Met Asn Pro Thr Gln Asn		
	385	390	395 400
15	Met Asp Met Pro Gln Leu Val Cys Pro Pro Val His Ser Glu Ser Arg		
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20	Leu Ala Gln Pro Asn Gln Val Pro Val Gln Pro Glu Ala Thr Gln Val		
	420	425	430
25	Pro Leu Val Ser Ser Thr Ser Glu Gly Tyr Thr Ala Ser Gln Pro Leu		
	435	440	445
30	Tyr Gln Pro Ser His Ala Thr Glu Gln Arg Pro Gln Lys Glu Pro Ile		
	450	455	460
35	Asp Gln Ile Gln Ala Thr Ile Ser Leu Asn Thr Asp Gln Thr Thr Ala		
	465	470	475 480
40	Ser Ser Ser Leu Pro Ala Ala Ser Gln Pro Gln Val Phe Gln Ala Gly		
	485	490	495
45	Thr Ser Lys Pro Leu His Ser Ser Gly Ile Asn Val Asn Ala Ala Pro		
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50	Phe Gln Ser Met Gln Thr Val Phe Asn Met Asn Ala Pro Val Pro Pro		
	515	520	525

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Val Asn Glu Pro Glu Thr Leu Lys Gln Gln Asn Gln Tyr Gln Ala Ser
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Tyr Asn Gln Ser Phe Ser Ser Gln Pro His Gln Val Glu Gln Thr Glu
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Leu Gln Gln Glu Gln Leu Gln Thr Val Val Gly Thr Tyr His Gly Ser
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Pro Asp Gln Ser His Gln Val Thr Gly Asn His Gln Gln Pro Pro Gln
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Gln Asn Thr Gly Phe Pro Arg Ser Asn Gln Pro Tyr Tyr Asn Ser Arg
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Gly Val Ser Arg Gly Gly Ser Arg Gly Ala Arg Gly Leu Met Asn Gly
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Tyr Arg Gly Pro Ala Asn Gly Phe Arg Gly Gly Tyr Asp Gly Tyr Arg
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Pro Ser Phe Ser Asn Thr Pro Asn Ser Gly Tyr Thr Gln Ser Gln Phe
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Ser Ala Pro Arg Asp Tyr Ser Gly Tyr Gln Arg Asp Gly Tyr Gln Gln
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Asn Phe Lys Arg Gly Ser Gly Gln Ser Gly Pro Arg Gly Ala Pro Arg
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Gly Arg Gly Gly Pro Pro Arg Pro Asn Arg Gly Met Pro Gln Met Asn

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40 Ser Gly Pro Pro Pro Pro Ser Gly Ser Ser Gly Ser Glu Ala Ala Ala
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Lys Lys Leu Arg Asn Leu Glu Lys Lys Lys Gly Lys Leu Asp Asp Tyr

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20	ata aag aag aca gca cgt cgg gag cag ctt atg aga gaa gaa gct gaa Ile Lys Lys Thr Ala Arg Arg Glu Gln Leu Met Arg Glu Glu Ala Glu 130 135 140	615		
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15	ccc ttg tac cag cct tct cat gct aca gag caa cga cca cag aag gaa Pro Leu Tyr Gln Pro Ser His Ala Thr Glu Gln Arg Pro Gln Lys Glu 450 455 460			1575
20	cca att gat cag att cag gca aca atc tct tta aat aca gac cag act Pro Ile Asp Gln Ile Gln Ala Thr Ile Ser Leu Asn Thr Asp Gln Thr 465 470 475			1623
25	aca gca tca tca tcc ctt cct gct gcg tct cag cct caa gta ttt cag Thr Ala Ser Ser Ser Leu Pro Ala Ala Ser Gln Pro Gln Val Phe Gln 480 485 490			1671
30	get ggg aca agc aaa cct tta cat agc agt gga atc aat gta aat gca Ala Gly Thr Ser Lys Pro Leu His Ser Ser Gly Ile Asn Val Asn Ala 495 500 505 510			1719
35	get cca ttc caa tcc atg caa acg gtg ttc aat atg aat gcc cca gtt Ala Pro Phe Gln Ser Met Gln Thr Val Phe Asn Met Asn Ala Pro Val 515 520 525			1767
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20	Leu Arg Asn Leu Glu Lys Lys Lys Gly Lys Leu Asp Asp Tyr Gln Glu	65	70	75
25	Arg Met Asn Lys Gly Glu Arg Leu Asn Gln Asp Gln Leu Asp Ala Val	85	90	95
30	Ser Lys Tyr Gln Glu Val Thr Asn Asn Leu Glu Phe Ala Lys Glu Leu	100	105	110
35	Gln Arg Ser Phe Met Ala Leu Ser Gln Asp Ile Gln Lys Thr Ile Lys	115	120	125
40	Lys Thr Ala Arg Arg Glu Gln Leu Met Arg Glu Glu Ala Glu Gln Lys	130	135	140
45	Arg Leu Lys Thr Val Leu Glu Leu Gln Tyr Val Leu Asp Lys Leu Gly	145	150	155
50	Asp Asp Glu Val Arg Thr Asp Leu Lys Gln Gly Leu Asn Gly Val Pro	165	170	175

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Ile Leu Ser Glu Glu Glu Leu Ser Leu Leu Asp Glu Phe Tyr Lys Leu
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Val Asp Pro Glu Arg Asp Met Ser Leu Arg Leu Asn Glu Gln Tyr Glu
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His Ala Ser Ile His Leu Trp Asp Leu Leu Glu Gly Lys Glu Lys Pro
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Val Cys Gly Thr Thr Tyr Lys Val Leu Lys Glu Ile Val Glu Arg Val
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Phe Gln Ser Asn Tyr Phe Asp Ser Thr His Asn His Gln Asn Gly Leu
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Cys Glu Glu Glu Glu Ala Ala Ser Ala Pro Ala Val Glu Asp Gln Val
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Pro Glu Ala Glu Pro Glu Pro Ala Glu Glu Tyr Thr Glu Gln Ser Glu
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Val Glu Ser Thr Glu Tyr Val Asn Arg Gln Phe Met Ala Glu Thr Gln
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Phe Thr Ser Gly Glu Lys Glu Gln Val Asp Glu Trp Thr Val Glu Thr
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Ser Val Pro Glu Pro His Ser Leu Thr Pro Val Ala Gln Ala Asp Pro
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15	Leu Asp Pro Ala Ile Val Ser Ala Gln Pro Met Asn Pro Thr Gln Asn	385	390	395
20	Met Asp Met Pro Gln Leu Val Cys Pro Pro Val His Ser Glu Ser Arg	405	410	415
25	Leu Ala Gln Pro Asn Gln Val Pro Val Gln Pro Glu Ala Thr Gln Val	420	425	430
30	Pro Leu Val Ser Ser Thr Ser Glu Gly Tyr Thr Ala Ser Gln Pro Leu	435	440	445
35	Tyr Gln Pro Ser His Ala Thr Glu Gln Arg Pro Gln Lys Glu Pro Ile	450	455	460
40	Asp Gln Ile Gln Ala Thr Ile Ser Leu Asn Thr Asp Gln Thr Thr Ala	465	470	475
45	Ser Ser Ser Leu Pro Ala Ala Ser Gln Pro Gln Val Phe Gln Ala Gly	485	490	495
50	Thr Ser Lys Pro Leu His Ser Ser Gly Ile Asn Val Asn Ala Ala Pro	500	505	510
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Tyr Asn Gln Ser Phe Ser Ser Gln Pro His Gln Val Glu Gln Thr Glu
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Leu Gln Gln Glu Gln Leu Gln Thr Val Val Gly Thr Tyr His Gly Ser
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	ggg tat aca gca tct caa ccc ttg tac cag cct tct cat gct aca gag	1065
	Gly Tyr Thr Ala Ser Gln Pro Leu Tyr Gln Pro Ser His Ala Thr Glu	
25	325 330 335 340	
	caa cga cca caa aag gaa cca att gac cag att cag gca aca atc tct	1113
	Gln Arg Pro Gln Lys Glu Pro Ile Asp Gln Ile Gln Ala Thr Ile Ser	
30	345 350 355	
	tta aat aca gac cag act aca gcg tca tca tcc ctt ccg gct gct tct	1161
	Leu Asn Thr Asp Gln Thr Thr Ala Ser Ser Ser Leu Pro Ala Ala Ser	
35	360 365 370	
	cag cct cag gta ttc cag gct ggg aca agc aaa cca tta cat agc agt	1209
	Gln Pro Gln Val Phe Gln Ala Gly Thr Ser Lys Pro Leu His Ser Ser	
40	375 380 385	
	gga atc aat gta aat gca gct cca ttc caa tcc atg caa acg gtg ttc	1257
	Gly Ile Asn Val Asn Ala Ala Pro Phe Gln Ser Met Gln Thr Val Phe	
45	390 395 400	
	aat atg aat gcc cca gtt cct cct gtt aat gaa cca gaa act ttg aaa	1305
	Asn Met Asn Ala Pro Val Pro Pro Val Asn Glu Pro Glu Thr Leu Lys	
50	405 410 415 420	
	caa caa aat cag tac cag gcc agt tat aac cag agc ttt tct agt cag	1353
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Gln Gln Asn Gln Tyr Gln Ala Ser Tyr Asn Gln Ser Phe Ser Ser Gln
425 430 435

5 cct cac caa gta gaa caa aca gag gga tgc cgc aaa tga acactcagca 1402
Pro His Gln Val Glu Gln Thr Glu Gly Cys Arg Lys
440 445

10 agtgaattaa tctgattcac aggattatgt ttaaacgccca aaaacacact ggccagtgtg 1462

ccataatatg ttaccagaag agttattatc tatttgttct ccctttcagg aaacttattg 1522

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Arg Glu Gln Leu Met Arg Glu Glu Ala Glu Gln Lys Arg Leu Lys Thr
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Val Leu Glu Leu Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp Glu Val
35 40 45

45

Arg Thr Asp Leu Lys Gln Gly Leu Asn Gly Val Pro Ile Leu Ser Glu
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50

Glu Glu Leu Ser Leu Leu Asp Glu Phe Tyr Lys Leu Ala Asp Pro Glu
65 70 75 80

55

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Arg Asp Met Ser Leu Arg Leu Asn Glu Gln Tyr Glu His Ala Ser Ile
85 90 95

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His Leu Trp Asp Leu Leu Glu Gly Lys Glu Lys Ser Val Cys Gly Thr
100 105 110

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Thr Tyr Lys Ala Leu Lys Glu Ile Val Glu Arg Val Phe Gln Ser Asn
115 120 125

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Tyr Phe Asp Ser Thr His Asn His Gln Asn Gly Leu Cys Glu Glu Glu
130 135 140

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Glu Ala Ala Ser Ala Pro Thr Val Glu Asp Gln Val Ala Glu Ala Glu
145 150 155 160

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Pro Glu Pro Ala Glu Glu Tyr Thr Glu Gln Ser Glu Val Glu Ser Thr
165 170 175

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Glu Tyr Val Asn Arg Gln Phe Met Ala Glu Thr Gln Phe Ser Ser Gly
180 185 190

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Glu Lys Glu Gln Val Asp Glu Trp Thr Val Glu Thr Val Glu Val Val
195 200 205

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Asn Ser Leu Gln Gln Gln Pro Gln Ala Ala Ser Pro Ser Val Pro Glu
210 215 220

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Pro His Ser Leu Thr Pro Val Ala Gln Ala Asp Pro Leu Val Arg Arg
225 230 235 240

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Gln Arg Val Gln Asp Leu Met Ala Gln Met Gln Gly Pro Tyr Asn Phe

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245

250

255

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Ile Gln Asp Ser Met Leu Asp Phe Glu Asn Gln Thr Leu Asp Pro Ala
260 265 270

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Ile Val Ser Ala Gln Pro Met Asn Pro Thr Gln Asn Met Asp Met Pro
275 280 285

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Gln Leu Val Cys Pro Pro Val His Ser Glu Ser Arg Leu Ala Gln Pro
290 295 300

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Asn Gln Val Pro Val Gln Pro Glu Ala Thr Gln Val Pro Leu Val Ser
305 310 315 320

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Ser Thr Ser Glu Gly Tyr Thr Ala Ser Gln Pro Leu Tyr Gln Pro Ser
325 330 335

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His Ala Thr Glu Gln Arg Pro Gln Lys Glu Pro Ile Asp Gln Ile Gln
340 345 350

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Ala Thr Ile Ser Leu Asn Thr Asp Gln Thr Thr Ala Ser Ser Ser Leu
355 360 365

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Pro Ala Ala Ser Gln Pro Gln Val Phe Gln Ala Gly Thr Ser Lys Pro
370 375 380

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Leu His Ser Ser Gly Ile Asn Val Asn Ala Ala Pro Phe Gln Ser Met
385 390 395 400

50

55

Gln Thr Val Phe Asn Met Asn Ala Pro Val Pro Pro Val Asn Glu Pro
405 410 415

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Glu Thr Leu Lys Gln Gln Asn Gln Tyr Gln Ala Ser Tyr Asn Gln Ser
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Phe Ser Ser Gln Pro His Gln Val Glu Gln Thr Glu Gly Cys Arg Lys
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ccg ccg ccc ccg tcg ggt tcc tcc ggg agc gag gcg gcg gcg gcg gcg 96
Pro Pro Pro Pro Ser Gly Ser Ser Gly Ser Glu Ala Ala Ala Ala Ala
20 25 30

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ggg gcg gcg ggg gcg gcg ggg gcc ggg gcg gct gcg ccc gcc tcc cag 144
Gly Ala Ala Gly Ala Ala Gly Ala Gly Ala Ala Ala Pro Ala Ser Gln
35 40 45

40

cac ccc gcg acc ggc acc ggc gct gtc cag acc gag gcc atg aag cag 192
His Pro Ala Thr Gly Thr Gly Ala Val Gln Thr Glu Ala Met Lys Gln
50 55 60

45

atc ctc ggg gtg atc gac aag aaa ctc cgg aac ctg gag aag aaa aag 240
Ile Leu Gly Val Ile Asp Lys Lys Leu Arg Asn Leu Glu Lys Lys Lys
65 70 75 80

50

ggc aag ctt gat gat tac cag gaa cga atg aac aaa ggg gaa agg ctt 288
Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg Leu

55

EP 2 733 492 A1

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10	aac ttg gag ttt gca aaa gaa tta cag agg agt ttc atg gca tta agt Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg Ser Phe Met Ala Leu Ser 115 120 125	384		
15	caa gat att cag aaa aca ata aag aag act gca cgt cgg gag cag ctt Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln Leu 130 135 140	432		
20	atg aga gag gaa gcg gaa caa aaa cgt tta aaa act gta ctt gag ctc Met Arg Glu Glu Ala Glu Gln Lys Arg Leu Lys Thr Val Leu Glu Leu 145 150 155 160	480		
25	cag tat gtt ttg gac aaa ttg gga gat gat gaa gtg aga act gac ctg Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp Glu Val Arg Thr Asp Leu 165 170 175	528		
30	aag caa ggt ttg aat gga gtg cca ata ttg tct gaa gaa gaa ttg tcg Lys Gln Gly Leu Asn Gly Val Pro Ile Leu Ser Glu Glu Glu Leu Ser 180 185 190	576		
35	ttg ttg gat gaa ttc tac aaa tta gca gac cct gaa cgg gac atg agc Leu Leu Asp Glu Phe Tyr Lys Leu Ala Asp Pro Glu Arg Asp Met Ser 195 200 205	624		
40	ttg agg ttg aat gag cag tat gaa cat gct tcc att cac ctg tgg gac Leu Arg Leu Asn Glu Gln Tyr Glu His Ala Ser Ile His Leu Trp Asp 210 215 220	672		
45	ttg ctg gaa gga aag gaa aag tct gta tgt gga aca acc tat aaa gca Leu Leu Glu Gly Lys Glu Lys Ser Val Cys Gly Thr Thr Tyr Lys Ala 225 230 235 240	720		
50	cta aag gaa att gtt gag cgt gtt ttc cag tca aat tac ttt gac agc Leu Lys Glu Ile Val Glu Arg Val Phe Gln Ser Asn Tyr Phe Asp Ser 245 250 255	768		

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	Thr His Asn His Gln Asn Gly Leu Cys Glu Glu Glu Glu Ala Ala Ser	
5	260 265 270	
	gca cct aca gtt gaa gac cag gta gct gaa gct gag cct gag cca gca	864
	Ala Pro Thr Val Glu Asp Gln Val Ala Glu Ala Glu Pro Glu Pro Ala	
10	275 280 285	
	gaa gaa tac act gaa caa agt gaa gtt gaa tca aca gag tat gta aat	912
	Glu Glu Tyr Thr Glu Gln Ser Glu Val Glu Ser Thr Glu Tyr Val Asn	
15	290 295 300	
	aga caa ttt atg gca gaa aca cag ttc agc agt ggt gaa aag gag cag	960
	Arg Gln Phe Met Ala Glu Thr Gln Phe Ser Ser Gly Glu Lys Glu Gln	
20	305 310 315 320	
	gta gat gag tgg acg gtc gaa aca gtg gag gtg gtg aat tca ctc cag	1008
	Val Asp Glu Trp Thr Val Glu Thr Val Glu Val Val Asn Ser Leu Gln	
25	325 330 335	
	cag caa cct cag gct gcg tct cct tca gta cca gag ccc cac tct ttg	1056
	Gln Gln Pro Gln Ala Ala Ser Pro Ser Val Pro Glu Pro His Ser Leu	
30	340 345 350	
	act ccg gtg gct cag gca gat ccc ctt gtg aga aga cag cga gtc cag	1104
	Thr Pro Val Ala Gln Ala Asp Pro Leu Val Arg Arg Gln Arg Val Gln	
35	355 360 365	
	gac ctt atg gcg cag atg cag ggg ccc tat aat ttc ata cag gat tca	1152
	Asp Leu Met Ala Gln Met Gln Gly Pro Tyr Asn Phe Ile Gln Asp Ser	
40	370 375 380	
	atg ctg gat ttt gaa aac cag aca ctc gat cct gcc att gta tct gca	1200
	Met Leu Asp Phe Glu Asn Gln Thr Leu Asp Pro Ala Ile Val Ser Ala	
45	385 390 395 400	
	cag cct atg aat ccg aca caa aac atg gac atg ccc cag ctg gtt tgc	1248
	Gln Pro Met Asn Pro Thr Gln Asn Met Asp Met Pro Gln Leu Val Cys	
50	405 410 415	
	cct cca gtt cat tct gaa tct aga ctt gct caa cct aat caa gtt cct	1296
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	435	440	445	
10	ggg tat aca gca tct caa ccc ttg tac cag cct tct cat gct aca gag Gly Tyr Thr Ala Ser Gln Pro Leu Tyr Gln Pro Ser His Ala Thr Glu	1392		
	450	455	460	
15	caa cga cca caa aag gaa cca att gac cag att cag gca aca atc tct Gln Arg Pro Gln Lys Glu Pro Ile Asp Gln Ile Gln Ala Thr Ile Ser	1440		
	465	470	475	480
20	tta aat aca gac cag act aca gcg tca tca tcc ctt ccg gct gct tct Leu Asn Thr Asp Gln Thr Thr Ala Ser Ser Ser Leu Pro Ala Ala Ser	1488		
	485	490	495	
25	cag cct cag gta ttc cag gct ggg aca agc aaa cca tta cat agc agt Gln Pro Gln Val Phe Gln Ala Gly Thr Ser Lys Pro Leu His Ser Ser	1536		
	500	505	510	
30	gga atc aat gta aat gca gct cca ttc caa tcc atg caa acg gtg ttc Gly Ile Asn Val Asn Ala Ala Pro Phe Gln Ser Met Gln Thr Val Phe	1584		
	515	520	525	
35	aat atg aat gcc cca gtt cct cct gtt aat gaa cca gaa act ttg aaa Asn Met Asn Ala Pro Val Pro Pro Val Asn Glu Pro Glu Thr Leu Lys	1632		
40	530	535	540	
45	caa caa aat cag tac cag gcc agt tat aac cag agc ttt tct agt cag Gln Gln Asn Gln Tyr Gln Ala Ser Tyr Asn Gln Ser Phe Ser Ser Gln	1680		
	545	550	555	560
50	cct cac caa gta gaa caa aca gac ctt cag caa gaa cag ctt caa aca Pro His Gln Val Glu Gln Thr Asp Leu Gln Gln Glu Gln Leu Gln Thr	1728		
	565	570	575	
55	gtg gtt ggc act tac cat ggt tcc cag gac cag ccc cac caa gtg act Val Val Gly Thr Tyr His Gly Ser Gln Asp Gln Pro His Gln Val Thr	1776		
	580	585	590	

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	ggt aac cat cag cag cct ccc cag cag aac act gga ttt cca cgt agc	1824
	Gly Asn His Gln Gln Pro Pro Gln Gln Asn Thr Gly Phe Pro Arg Ser	
	595 600 605	
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	agt cag ccc tat tac aat agt cgt ggt gtg tct cgt ggt ggt tcc cgt	1872
	Ser Gln Pro Tyr Tyr Asn Ser Arg Gly Val Ser Arg Gly Gly Ser Arg	
10	610 615 620	
	ggt gct aga ggc tta atg aat gga tac agg ggc cct gcc aat gga ttc	1920
	Gly Ala Arg Gly Leu Met Asn Gly Tyr Arg Gly Pro Ala Asn Gly Phe	
15	625 630 635 640	
	aga gga gga tat gat ggt tac cgc cct tca ttc tct aac act cca aac	1968
	Arg Gly Gly Tyr Asp Gly Tyr Arg Pro Ser Phe Ser Asn Thr Pro Asn	
20	645 650 655	
	agt ggt tat aca cag tct cag ttc agt gct ccc cgg gac tac tct ggc	2016
	Ser Gly Tyr Thr Gln Ser Gln Phe Ser Ala Pro Arg Asp Tyr Ser Gly	
25	660 665 670	
	tat cag cgg gat gga tat cag cag aat ttc aag cga ggc tct ggg cag	2064
	Tyr Gln Arg Asp Gly Tyr Gln Gln Asn Phe Lys Arg Gly Ser Gly Gln	
30	675 680 685	
	agt gga cca cgg gga gcc cca cga ggt cgt gga ggg ccc cca aga ccc	2112
	Ser Gly Pro Arg Gly Ala Pro Arg Gly Arg Gly Gly Pro Pro Arg Pro	
35	690 695 700	
	aac aga ggg atg ccg caa atg aac act cag caa gtg aat taa	2154
	Asn Arg Gly Met Pro Gln Met Asn Thr Gln Gln Val Asn	
40	705 710 715	
	tctgattcac aggattatgt ttaaagcca aaaacacact ggccagtgtg ccataatatg	2214
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	ttaccagaag agttattatc tatttggttct ccttttcagg aaacttattg taaagggact	2274
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	gttttcatcc cataaagaca ggactacaat tgtcagcttt atattacctg gatatggaag	2334
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5 acaaatcagc cctagagTTa ttcaaatggT aattgacaaa aactaaaata ttTccctTcg 2574

agaaggagtG gaatgtggTT tggcagaaca actgcattTc acagctTtTc cggTTaaatt 2634

10 ggagcactaa acgTTtagat gcataccaaa ttatgcatgg gccTTtaata taaaaggctG 2694

gctaccagct ttgacacagc actattcatc ctctggccaa acaactgtgg ttaaacaaca 2754

15 catgtaaatt gctTTTTaTc agctgatact ataataagac aaagccaaaa tgcaaaaatt 2814

gggctTtgat tggcactTTT tgaaaaatat gcaacaaata tgggatgTaa tctggatggc 2874

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gacaatgact tTtgTaaGga tTggTactat ctatcattcc tTataatgTa cattgtctgt 2994

25 cactaatcct cagatctTgc tgtattgtca cctaaattgg tacaggTact gatgaaaata 3054

tctaatggat aatcataaca ctctTggTca catgTTTtTc ctgcagcctG aaggTTTtTa 3114

30 aaagaaaaag atatcaaatG cctgtctgTa ccacctTTT aaattgctat cTTTtgaaaa 3174

gcaccagtat gtgTTTtaga tTgattTccc tattTtaggg aaatgacaga cagtagTtTc 3234

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ctggTgtTca acagctagca gcttatgtgg tTcaccccat gcattgttag tgtTtcagat 3354

40 tTtatggTta tctccagcag ctgTtTctgt agtactTgca tTtatctTTT gtctaaccct 3414

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EP 2 733 492 A1

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 ttgaacattc cacattcaaa agttttttgt aggggtggtg ggaagggggg gtgtcttcaa 3894
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40 Pro Pro Pro Pro Ser Gly Ser Ser Gly Ser Glu Ala Ala Ala Ala Ala
 20 25 30

45 Gly Ala Ala Gly Ala Ala Gly Ala Gly Ala Ala Ala Pro Ala Ser Gln
 35 40 45

50 His Pro Ala Thr Gly Thr Gly Ala Val Gln Thr Glu Ala Met Lys Gln
 50 55 60

55 Ile Leu Gly Val Ile Asp Lys Lys Leu Arg Asn Leu Glu Lys Lys Lys
 65 70 75 80

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	Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg Leu	
	85	90 95
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	Asn Gln Asp Gln Leu Asp Ala Val Ser Lys Tyr Gln Glu Val Thr Asn	
	100	105 110
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	Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg Ser Phe Met Ala Leu Ser	
	115	120 125
15		
	Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln Leu	
	130	135 140
20		
	Met Arg Glu Glu Ala Glu Gln Lys Arg Leu Lys Thr Val Leu Glu Leu	
	145	150 155 160
25		
	Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp Glu Val Arg Thr Asp Leu	
	165	170 175
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	Lys Gln Gly Leu Asn Gly Val Pro Ile Leu Ser Glu Glu Glu Leu Ser	
	180	185 190
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	Leu Leu Asp Glu Phe Tyr Lys Leu Ala Asp Pro Glu Arg Asp Met Ser	
	195	200 205
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	Leu Arg Leu Asn Glu Gln Tyr Glu His Ala Ser Ile His Leu Trp Asp	
	210	215 220
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	Leu Leu Glu Gly Lys Glu Lys Ser Val Cys Gly Thr Thr Tyr Lys Ala	
	225	230 235 240
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Leu Lys Glu Ile Val Glu Arg Val Phe Gln Ser Asn Tyr Phe Asp Ser
245 250 255

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Thr His Asn His Gln Asn Gly Leu Cys Glu Glu Glu Glu Ala Ala Ser
260 265 270

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Ala Pro Thr Val Glu Asp Gln Val Ala Glu Ala Glu Pro Glu Pro Ala
275 280 285

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Glu Glu Tyr Thr Glu Gln Ser Glu Val Glu Ser Thr Glu Tyr Val Asn
290 295 300

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Arg Gln Phe Met Ala Glu Thr Gln Phe Ser Ser Gly Glu Lys Glu Gln
305 310 315 320

25

Val Asp Glu Trp Thr Val Glu Thr Val Glu Val Val Asn Ser Leu Gln
325 330 335

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Gln Gln Pro Gln Ala Ala Ser Pro Ser Val Pro Glu Pro His Ser Leu
340 345 350

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Thr Pro Val Ala Gln Ala Asp Pro Leu Val Arg Arg Gln Arg Val Gln
355 360 365

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Asp Leu Met Ala Gln Met Gln Gly Pro Tyr Asn Phe Ile Gln Asp Ser
370 375 380

45

Met Leu Asp Phe Glu Asn Gln Thr Leu Asp Pro Ala Ile Val Ser Ala
385 390 395 400

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Gln Pro Met Asn Pro Thr Gln Asn Met Asp Met Pro Gln Leu Val Cys
405 410 415

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EP 2 733 492 A1

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10	Val Gln Pro Glu Ala Thr Gln Val Pro Leu Val Ser Ser Thr Ser Glu	435	440	445	
15	Gly Tyr Thr Ala Ser Gln Pro Leu Tyr Gln Pro Ser His Ala Thr Glu	450	455	460	
20	Gln Arg Pro Gln Lys Glu Pro Ile Asp Gln Ile Gln Ala Thr Ile Ser	465	470	475	480
25	Leu Asn Thr Asp Gln Thr Thr Ala Ser Ser Ser Leu Pro Ala Ala Ser	485	490	495	
30	Gln Pro Gln Val Phe Gln Ala Gly Thr Ser Lys Pro Leu His Ser Ser	500	505	510	
35	Gly Ile Asn Val Asn Ala Ala Pro Phe Gln Ser Met Gln Thr Val Phe	515	520	525	
40	Asn Met Asn Ala Pro Val Pro Pro Val Asn Glu Pro Glu Thr Leu Lys	530	535	540	
45	Gln Gln Asn Gln Tyr Gln Ala Ser Tyr Asn Gln Ser Phe Ser Ser Gln	545	550	555	560
50	Pro His Gln Val Glu Gln Thr Asp Leu Gln Gln Glu Gln Leu Gln Thr	565	570	575	

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Val Val Gly Thr Tyr His Gly Ser Gln Asp Gln Pro His Gln Val Thr
580 585 590

5

Gly Asn His Gln Gln Pro Pro Gln Gln Asn Thr Gly Phe Pro Arg Ser
595 600 605

10

Ser Gln Pro Tyr Tyr Asn Ser Arg Gly Val Ser Arg Gly Gly Ser Arg
610 615 620

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Gly Ala Arg Gly Leu Met Asn Gly Tyr Arg Gly Pro Ala Asn Gly Phe
625 630 635 640

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Arg Gly Gly Tyr Asp Gly Tyr Arg Pro Ser Phe Ser Asn Thr Pro Asn
645 650 655

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Ser Gly Tyr Thr Gln Ser Gln Phe Ser Ala Pro Arg Asp Tyr Ser Gly
660 665 670

30

Tyr Gln Arg Asp Gly Tyr Gln Gln Asn Phe Lys Arg Gly Ser Gly Gln
675 680 685

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Ser Gly Pro Arg Gly Ala Pro Arg Gly Arg Gly Gly Pro Pro Arg Pro
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Asn Arg Gly Met Pro Gln Met Asn Thr Gln Gln Val Asn
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EP 2 733 492 A1

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ccg ccg ccc ccg tcg ggt tcc tcc ggg agc gag gcg gcg gcg gcg gcg 96
Pro Pro Pro Pro Ser Gly Ser Ser Gly Ser Glu Ala Ala Ala Ala Ala
20 25 30

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ggg gcg gcg ggg gcg gcg ggg gcc ggg gcg gct gcg ccc gcc tcc cag 144
Gly Ala Ala Gly Ala Ala Gly Ala Gly Ala Ala Ala Pro Ala Ser Gln
35 40 45

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cac ccc gcg acc ggc acc ggc gct gtc cag acc gag gcc atg aag cag 192
His Pro Ala Thr Gly Thr Gly Ala Val Gln Thr Glu Ala Met Lys Gln
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atc ctc ggg gtg atc gac aag aaa ctc cgg aac ctg gag aag aaa aag 240
Ile Leu Gly Val Ile Asp Lys Lys Leu Arg Asn Leu Glu Lys Lys Lys
65 70 75 80

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ggc aag ctt gat gat tac cag gaa cga atg aac aaa ggg gaa agg ctt 288
Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg Leu
85 90 95

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aat caa gat cag ctg gat gcc gta tct aag tac cag gaa gtc aca aat 336
Asn Gln Asp Gln Leu Asp Ala Val Ser Lys Tyr Gln Glu Val Thr Asn
100 105 110

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aac ttg gag ttt gca aaa gaa tta cag agg agt ttc atg gca tta agt 384
Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg Ser Phe Met Ala Leu Ser
115 120 125

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caa gat att cag aaa aca ata aag aag act gca cgt cgg gag cag ctt 432
Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln Leu
130 135 140

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atg aga gag gaa gcg gaa caa aaa cgt tta aaa act gta ctt gag ctc 480

EP 2 733 492 A1

	Met Arg Glu Glu Ala Glu Gln Lys Arg Leu Lys Thr Val Leu Glu Leu	
	145 150 155 160	
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	Lys Gln Gly Leu Asn Gly Val Pro Ile Leu Ser Glu Glu Glu Leu Ser	
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	Leu Leu Asp Glu Phe Tyr Lys Leu Ala Asp Pro Glu Arg Asp Met Ser	
	195 200 205	
20	ttg agg ttg aat gag cag tat gaa cat gct tcc att cac ctg tgg gac	672
	Leu Arg Leu Asn Glu Gln Tyr Glu His Ala Ser Ile His Leu Trp Asp	
	210 215 220	
25	ttg ctg gaa gga aag gaa aag tct gta tgt gga aca acc tat aaa gca	720
	Leu Leu Glu Gly Lys Glu Lys Ser Val Cys Gly Thr Thr Tyr Lys Ala	
30	225 230 235 240	
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	Leu Lys Glu Ile Val Glu Arg Val Phe Gln Ser Asn Tyr Phe Asp Ser	
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	act cac aac cac cag aat ggg cta tgt gag gaa gaa gag gca gcc tca	816
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	gca cct aca gtt gaa gac cag gta gct gaa gct gag cct gag cca gca	864
	Ala Pro Thr Val Glu Asp Gln Val Ala Glu Ala Glu Pro Glu Pro Ala	
45	275 280 285	
	gaa gaa tac act gaa caa agt gaa gtt gaa tca aca gag tat gta aat	912
	Glu Glu Tyr Thr Glu Gln Ser Glu Val Glu Ser Thr Glu Tyr Val Asn	
50	290 295 300	
	aga caa ttt atg gca gaa aca cag ttc agc agt ggt gaa aag gag cag	960
	Arg Gln Phe Met Ala Glu Thr Gln Phe Ser Ser Gly Glu Lys Glu Gln	
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	Leu Asn Thr Asp Gln Thr Thr Ala Ser Ser Ser Leu Pro Ala Ala Ser	
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	500 505 510	
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15	Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg Leu				
		85		90	95
20	Asn Gln Asp Gln Leu Asp Ala Val Ser Lys Tyr Gln Glu Val Thr Asn				
		100		105	110
25	Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg Ser Phe Met Ala Leu Ser				
		115		120	125
30	Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln Leu				
		130		135	140
35	Met Arg Glu Glu Ala Glu Gln Lys Arg Leu Lys Thr Val Leu Glu Leu				
		145		150	155 160
40	Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp Glu Val Arg Thr Asp Leu				
		165		170	175
45	Lys Gln Gly Leu Asn Gly Val Pro Ile Leu Ser Glu Glu Glu Leu Ser				
		180		185	190
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Leu Arg Leu Asn Glu Gln Tyr Glu His Ala Ser Ile His Leu Trp Asp
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Leu Leu Glu Gly Lys Glu Lys Ser Val Cys Gly Thr Thr Tyr Lys Ala
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Leu Lys Glu Ile Val Glu Arg Val Phe Gln Ser Asn Tyr Phe Asp Ser
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Thr His Asn His Gln Asn Gly Leu Cys Glu Glu Glu Glu Ala Ala Ser
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Ala Pro Thr Val Glu Asp Gln Val Ala Glu Ala Glu Pro Glu Pro Ala
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Glu Glu Tyr Thr Glu Gln Ser Glu Val Glu Ser Thr Glu Tyr Val Asn
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Arg Gln Phe Met Ala Glu Thr Gln Phe Ser Ser Gly Glu Lys Glu Gln
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Val Asp Glu Trp Thr Val Glu Thr Val Glu Val Val Asn Ser Leu Gln
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Gln Gln Pro Gln Ala Ala Ser Pro Ser Val Pro Glu Pro His Ser Leu
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Thr Pro Val Ala Gln Ala Asp Pro Leu Val Arg Arg Gln Arg Val Gln
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			435					440						445		
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		450						455					460			
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	465					470					475				480	
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					485						490				495	
40	Gln	Pro	Gln	Val	Phe	Gln	Ala	Gly	Thr	Ser	Lys	Pro	Leu	His	Ser	Ser
				500					505					510		
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		515						520					525			
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	530							535					540			
55																

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Gln Gln Asn Gln Tyr Gln Ala Ser Tyr Asn Gln Ser Phe Ser Ser Gln
545 550 555 560

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Pro His Gln Val Glu Gln Thr Asp Leu Gln Gln Glu Gln Leu Gln Thr
565 570 575

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Val Val Gly Thr Tyr His Gly Ser Gln Asp Gln Pro His Gln Val Thr
580 585 590

15

Gly Asn His Gln Gln Pro Pro Gln Gln Asn Thr Gly Phe Pro Arg Ser
595 600 605

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Ser Gln Pro Tyr Tyr Asn Ser Arg Gly Val Ser Arg Gly Gly Ser Arg
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Gly Ala Arg Gly Leu Met Asn Gly Tyr Arg Gly Pro Ala Asn Gly Phe
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Arg Gly Gly Tyr Asp Gly Tyr Arg Pro Ser Phe Ser Asn Thr Pro Asn
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 Gly Ala Ala Gly Ala Ala Gly Ala Gly Ala Ala Ala Pro Ala Ser Gln
 35 40 45

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 His Pro Ala Thr Gly Thr Gly Ala Val Gln Thr Glu Ala Met Lys Gln
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 Ile Leu Gly Val Ile Asp Lys Lys Leu Arg Asn Leu Glu Lys Lys Lys
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 85 90 95

aat caa gat cag ctg gat gcc gta tct aag tac cag gaa gtc aca aat 336
 Asn Gln Asp Gln Leu Asp Ala Val Ser Lys Tyr Gln Glu Val Thr Asn
 100 105 110

aac ttg gag ttt gca aaa gaa tta cag agg agt ttc atg gca tta agt 384
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40	cct cca gtt cat tct gaa tct aga ctt gct caa cct aat caa gtt cct Pro Pro Val His Ser Glu Ser Arg Leu Ala Gln Pro Asn Gln Val Pro 420 425 430			1296
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45	ggt aac cat cag cag cct ccc cag cag aac act gga ttt cca cgt agc Gly Asn His Gln Gln Pro Pro Gln Gln Asn Thr Gly Phe Pro Arg Ser 595 600 605	1824
50	agt cag ccc tat tac aat agt cgt ggt gtg tct cgt ggt ggt tcc cgt Ser Gln Pro Tyr Tyr Asn Ser Arg Gly Val Ser Arg Gly Gly Ser Arg 610 615 620	1872
55	ggt gct aga ggc tta atg aat gga tac agg ggc cct gcc aat gga ttc Gly Ala Arg Gly Leu Met Asn Gly Tyr Arg Gly Pro Ala Asn Gly Phe	1920

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	625	630	635	640	
5	aga gga gga tat gat ggt tac cgc cct tca ttc tct aac act cca aac				1968
	Arg Gly Gly Tyr Asp Gly Tyr Arg Pro Ser Phe Ser Asn Thr Pro Asn				
		645	650	655	
10	agt ggt tat aca cag tct cag ttc agt gct ccc cgg gac tac tct ggc				2016
	Ser Gly Tyr Thr Gln Ser Gln Phe Ser Ala Pro Arg Asp Tyr Ser Gly				
		660	665	670	
15	tat cag cgg gga tgc cgc aaa tga aactcagca agtgaattaa tctgattcac				2070
	Tyr Gln Arg Gly Cys Arg Lys				
		675			
20	aggattatgt ttaaacgccca aaaacacact ggccagtgtta ccataatatg ttaccagaag				2130
	agttattatc tatttgttct cccttcagg aaacttattg taaagggact gttttcatcc				2190
25	cataaagaca ggactacaat tgtcagcttt atattacctg gatatggaag gaaactattt				2250
	ttattctgca tgttttctt aagcgtcatc ttgagccttg cacatgatac tcagattcct				2310
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	gaagtggctt ggaaaaagca agattaactt ctgacattgg ataaaaatca acaaatcagc				2430
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	acgttttagat gcataccaaa ttatgcatgg gcccttaata taaaaggctg gctaccagct				2610
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cagatcttgc tgtattgtca cctaaattgg tacaggtact gatgaaaata tctaattgat 2970

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atatcaaag cctgctgcta ccaccctttt aaattgctat cttttgaaaa gcaccagtat 3090

10 gtgtttttaga ttgatttccc tattttaggg aaatgacaga cagtagtttc agttctgatg 3150

gtataagcaa aacaaataaa acatgtttat aaaagttgta tcttgaaaca ctggtgttca 3210

15 acagctagca gcttatgtgg ttcaccccat gcattgttag tgtttcagat tttatggta 3270

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Gly Ala Ala Gly Ala Ala Gly Ala Gly Ala Ala Ala Pro Ala Ser Gln

35 40 45

45

His Pro Ala Thr Gly Thr Gly Ala Val Gln Thr Glu Ala Met Lys Gln

50 55 60

55

Ile Leu Gly Val Ile Asp Lys Lys Leu Arg Asn Leu Glu Lys Lys Lys

65 70 75 80

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Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg Leu
85 90 95

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Asn Gln Asp Gln Leu Asp Ala Val Ser Lys Tyr Gln Glu Val Thr Asn
100 105 110

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Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg Ser Phe Met Ala Leu Ser
115 120 125

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Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln Leu
130 135 140

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Met Arg Glu Glu Ala Glu Gln Lys Arg Leu Lys Thr Val Leu Glu Leu
145 150 155 160

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Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp Glu Val Arg Thr Asp Leu
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Lys Gln Gly Leu Asn Gly Val Pro Ile Leu Ser Glu Glu Glu Leu Ser
180 185 190

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Leu Leu Asp Glu Phe Tyr Lys Leu Ala Asp Pro Glu Arg Asp Met Ser
195 200 205

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Leu Arg Leu Asn Glu Gln Tyr Glu His Ala Ser Ile His Leu Trp Asp
210 215 220

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Leu Leu Glu Gly Lys Glu Lys Ser Val Cys Gly Thr Thr Tyr Lys Ala
225 230 235 240

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Leu Lys Glu Ile Val Glu Arg Val Phe Gln Ser Asn Tyr Phe Asp Ser
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55

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	Thr His Asn His Gln Asn Gly Leu Cys Glu Glu Glu Glu Ala Ala Ser	
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	Ala Pro Thr Val Glu Asp Gln Val Ala Glu Ala Glu Pro Glu Pro Ala	
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	Glu Glu Tyr Thr Glu Gln Ser Glu Val Glu Ser Thr Glu Tyr Val Asn	
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15		
	Arg Gln Phe Met Ala Glu Thr Gln Phe Ser Ser Gly Glu Lys Glu Gln	
	305	310 315 320
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	Val Asp Glu Trp Thr Val Glu Thr Val Glu Val Val Asn Ser Leu Gln	
	325	330 335
25		
	Gln Gln Pro Gln Ala Ala Ser Pro Ser Val Pro Glu Pro His Ser Leu	
	340	345 350
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	Thr Pro Val Ala Gln Ala Asp Pro Leu Val Arg Arg Gln Arg Val Gln	
	355	360 365
35		
	Asp Leu Met Ala Gln Met Gln Gly Pro Tyr Asn Phe Ile Gln Asp Ser	
	370	375 380
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	Met Leu Asp Phe Glu Asn Gln Thr Leu Asp Pro Ala Ile Val Ser Ala	
	385	390 395 400
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	Gln Pro Met Asn Pro Thr Gln Asn Met Asp Met Pro Gln Leu Val Cys	
	405	410 415
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55		

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Pro Pro Val His Ser Glu Ser Arg Leu Ala Gln Pro Asn Gln Val Pro
420 425 430

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Val Gln Pro Glu Ala Thr Gln Val Pro Leu Val Ser Ser Thr Ser Glu
435 440 445

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Gly Tyr Thr Ala Ser Gln Pro Leu Tyr Gln Pro Ser His Ala Thr Glu
450 455 460

15

Gln Arg Pro Gln Lys Glu Pro Ile Asp Gln Ile Gln Ala Thr Ile Ser
465 470 475 480

20

Leu Asn Thr Asp Gln Thr Thr Ala Ser Ser Ser Leu Pro Ala Ala Ser
485 490 495

25

Gln Pro Gln Val Phe Gln Ala Gly Thr Ser Lys Pro Leu His Ser Ser
500 505 510

30

Gly Ile Asn Val Asn Ala Ala Pro Phe Gln Ser Met Gln Thr Val Phe
515 520 525

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Asn Met Asn Ala Pro Val Pro Pro Val Asn Glu Pro Glu Thr Leu Lys
530 535 540

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Gln Gln Asn Gln Tyr Gln Ala Ser Tyr Asn Gln Ser Phe Ser Ser Gln
545 550 555 560

45

Pro His Gln Val Glu Gln Thr Asp Leu Gln Gln Glu Gln Leu Gln Thr
565 570 575

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Val Val Gly Thr Tyr His Gly Ser Gln Asp Gln Pro His Gln Val Thr
580 585 590

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5 Gly Asn His Gln Gln Pro Pro Gln Gln Asn Thr Gly Phe Pro Arg Ser
595 600 605

10 Ser Gln Pro Tyr Tyr Asn Ser Arg Gly Val Ser Arg Gly Gly Ser Arg
610 615 620

15 Gly Ala Arg Gly Leu Met Asn Gly Tyr Arg Gly Pro Ala Asn Gly Phe
625 630 635 640

20 Arg Gly Gly Tyr Asp Gly Tyr Arg Pro Ser Phe Ser Asn Thr Pro Asn
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25 Ser Gly Tyr Thr Gln Ser Gln Phe Ser Ala Pro Arg Asp Tyr Ser Gly
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30 Tyr Gln Arg Gly Cys Arg Lys
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40 <213> Canis familiaris

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	35 40 45	
10	cac ccc gcg acc ggc acc ggc gct gtc cag acc gag gcc atg aag cag His Pro Ala Thr Gly Thr Gly Ala Val Gln Thr Glu Ala Met Lys Gln	192
	50 55 60	
15	atc ctc ggg gtg atc gac aag aaa ctc cgg aac ctg gag aag aaa aag Ile Leu Gly Val Ile Asp Lys Lys Leu Arg Asn Leu Glu Lys Lys Lys	240
	65 70 75 80	
20	ggc aag ctt gat gat tac cag gaa cga atg aac aaa ggg gaa agg ctt Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg Leu	288
	85 90 95	
25	aat caa gat cag ctg gat gcc gta tct aag tac cag gaa gtc aca aat Asn Gln Asp Gln Leu Asp Ala Val Ser Lys Tyr Gln Glu Val Thr Asn	336
	100 105 110	
30	aac ttg gag ttt gca aaa gaa tta cag agg agt ttc atg gca tta agt Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg Ser Phe Met Ala Leu Ser	384
	115 120 125	
35	caa gat att cag aaa aca ata aag aag act gca cgt cgg gag cag ctt Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln Leu	432
	130 135 140	
40	atg aga gag gaa gcg gaa caa aaa cgt tta aaa act gta ctt gag ctc Met Arg Glu Glu Ala Glu Gln Lys Arg Leu Lys Thr Val Leu Glu Leu	480
	145 150 155 160	
45	cag tat gtt ttg gac aaa ttg gga gat gat gaa gtg aga act gac ctg Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp Glu Val Arg Thr Asp Leu	528
	165 170 175	
50	aag caa ggt ttg aat gga gtg cca ata ttg tct gaa gaa gaa ttg tcg Lys Gln Gly Leu Asn Gly Val Pro Ile Leu Ser Glu Glu Glu Leu Ser	576
	180 185 190	
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10	ttg agg ttg aat gag cag tat gaa cat gct tcc att cac ctg tgg gac Leu Arg Leu Asn Glu Gln Tyr Glu His Ala Ser Ile His Leu Trp Asp 210 215 220	672
15	ttg ctg gaa gga aag gaa aag tct gta tgt gga aca acc tat aaa gca Leu Leu Glu Gly Lys Glu Lys Ser Val Cys Gly Thr Thr Tyr Lys Ala 225 230 235 240	720
20	cta aag gaa att gtt gag cgt gtt ttc cag tca aat tac ttt gac agc Leu Lys Glu Ile Val Glu Arg Val Phe Gln Ser Asn Tyr Phe Asp Ser 245 250 255	768
25	act cac aac cac cag aat ggg cta tgt gag gaa gaa gag gca gcc tca Thr His Asn His Gln Asn Gly Leu Cys Glu Glu Glu Glu Ala Ala Ser 260 265 270	816
30	gca cct aca gtt gaa gac cag gta gct gaa gct gag cct gag cca gca Ala Pro Thr Val Glu Asp Gln Val Ala Glu Ala Glu Pro Glu Pro Ala 275 280 285	864
35	gaa gaa tac act gaa caa agt gaa gtt gaa tca aca gag tat gta aat Glu Glu Tyr Thr Glu Gln Ser Glu Val Glu Ser Thr Glu Tyr Val Asn 290 295 300	912
40	aga caa ttt atg gca gaa aca cag ttc agc agt ggt gaa aag gag cag Arg Gln Phe Met Ala Glu Thr Gln Phe Ser Ser Gly Glu Lys Glu Gln 305 310 315 320	960
45	gta gat gag tgg acg gtc gaa aca gtg gag gtg gtg aat tca ctc cag Val Asp Glu Trp Thr Val Glu Thr Val Glu Val Val Asn Ser Leu Gln 325 330 335	1008
50	cag caa cct cag gct gcg tct cct tca gta cca gag ccc cac tct ttg Gln Gln Pro Gln Ala Ala Ser Pro Ser Val Pro Glu Pro His Ser Leu 340 345 350	1056
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	Thr Pro Val Ala Gln Ala Asp Pro Leu Val Arg Arg Gln Arg Val Gln	
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	370 375 380	
10	atg ctg gat ttt gaa aac cag aca ctc gat cct gcc att gta tct gca Met Leu Asp Phe Glu Asn Gln Thr Leu Asp Pro Ala Ile Val Ser Ala	1200
	385 390 395 400	
15	cag cct atg aat ccg aca caa aac atg gac atg ccc cag ctg gtt tgc Gln Pro Met Asn Pro Thr Gln Asn Met Asp Met Pro Gln Leu Val Cys	1248
	405 410 415	
20	cct cca gtt cat tct gaa tct aga ctt gct caa cct aat caa gtt cct Pro Pro Val His Ser Glu Ser Arg Leu Ala Gln Pro Asn Gln Val Pro	1296
	420 425 430	
25	gta caa cca gaa gct aca cag gtt cct ttg gtt tca tcc aca agt gag Val Gln Pro Glu Ala Thr Gln Val Pro Leu Val Ser Ser Thr Ser Glu	1344
	435 440 445	
30	ggg tat aca gca tct caa ccc ttg tac cag cct tct cat gct aca gag Gly Tyr Thr Ala Ser Gln Pro Leu Tyr Gln Pro Ser His Ala Thr Glu	1392
	450 455 460	
35	caa cga cca caa aag gaa cca att gac cag att cag gca aca atc tct Gln Arg Pro Gln Lys Glu Pro Ile Asp Gln Ile Gln Ala Thr Ile Ser	1440
	465 470 475 480	
40	tta aat aca gac cag act aca gcg tca tca tcc ctt ccg gct gct tct Leu Asn Thr Asp Gln Thr Thr Ala Ser Ser Ser Leu Pro Ala Ala Ser	1488
	485 490 495	
45	cag cct cag gta ttc cag gct ggg aca agc aaa cca tta cat agc agt Gln Pro Gln Val Phe Gln Ala Gly Thr Ser Lys Pro Leu His Ser Ser	1536
	500 505 510	
50	gga atc aat gta aat gca gct cca ttc caa tcc atg caa acg gtg ttc Gly Ile Asn Val Asn Ala Ala Pro Phe Gln Ser Met Gln Thr Val Phe	1584
	515 520 525	
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10	caa caa aat cag tac cag gcc agt tat aac cag agc ttt tct agt cag Gln Gln Asn Gln Tyr Gln Ala Ser Tyr Asn Gln Ser Phe Ser Ser Gln 545 550 555 560	1680
15	cct cac caa gta gaa caa aca gac ctt cag caa gaa cag ctt caa aca Pro His Gln Val Glu Gln Thr Asp Leu Gln Gln Glu Gln Leu Gln Thr 565 570 575	1728
20	gtg gtt ggc act tac cat ggt tcc cag gac cag ccc cac caa gtg act Val Val Gly Thr Tyr His Gly Ser Gln Asp Gln Pro His Gln Val Thr 580 585 590	1776
25	ggt aac cat cag cag cct ccc cag cag aac act gga ttt cca cgt agc Gly Asn His Gln Gln Pro Pro Gln Gln Asn Thr Gly Phe Pro Arg Ser 595 600 605	1824
30	agt cag ccc tat tac aat agt cgt ggt gtg tct cgt ggt ggt tcc cgt Ser Gln Pro Tyr Tyr Asn Ser Arg Gly Val Ser Arg Gly Gly Ser Arg 610 615 620	1872
35	ggt gct aga ggc tta atg aat gga tac agg ggc cct gcc aat gga ttc Gly Ala Arg Gly Leu Met Asn Gly Tyr Arg Gly Pro Ala Asn Gly Phe 625 630 635 640	1920
40	aga gga gga tat gat ggt tac cgc cct tca ttc tct aac act cca aac Arg Gly Gly Tyr Asp Gly Tyr Arg Pro Ser Phe Ser Asn Thr Pro Asn 645 650 655	1968
45	agt ggt tat aca cag tct cag ttc agt gct ccc cgg gac tac tct ggc Ser Gly Tyr Thr Gln Ser Gln Phe Ser Ala Pro Arg Asp Tyr Ser Gly 660 665 670	2016
50	tat cag cgg gat gga tat cag cag aat ttc aag cga ggc tct ggg cag Tyr Gln Arg Asp Gly Tyr Gln Gln Asn Phe Lys Arg Gly Ser Gly Gln 675 680 685	2064
55	agt gga cca cgg gga gcc cca cga ggt cgt gga ggg ccc cca aga ccc	2112

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690 695 700

5 aac aga ggg atg ccg caa atg aac act cag caa gtg aat taa 2154
Asn Arg Gly Met Pro Gln Met Asn Thr Gln Gln Val Asn
705 710 715

10 tctgattcac aggattatgt ttaaacgccca aaaacacact ggccagtgtta ccataatatg 2214
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15 tgtcagc 2281

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40 Gly Ala Ala Gly Ala Ala Gly Ala Gly Ala Ala Ala Pro Ala Ser Gln
35 40 45

45 His Pro Ala Thr Gly Thr Gly Ala Val Gln Thr Glu Ala Met Lys Gln
50 55 60

50 Ile Leu Gly Val Ile Asp Lys Lys Leu Arg Asn Leu Glu Lys Lys Lys
65 70 75 80

55 Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg Leu

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5	Asn Gln Asp Gln Leu Asp Ala Val Ser Lys Tyr Gln Glu Val Thr Asn		
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10	Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg Ser Phe Met Ala Leu Ser		
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15	Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln Leu		
	130	135	140
20	Met Arg Glu Glu Ala Glu Gln Lys Arg Leu Lys Thr Val Leu Glu Leu		
	145	150	155
25	Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp Glu Val Arg Thr Asp Leu		
	165	170	175
30	Lys Gln Gly Leu Asn Gly Val Pro Ile Leu Ser Glu Glu Glu Leu Ser		
	180	185	190
35	Leu Leu Asp Glu Phe Tyr Lys Leu Ala Asp Pro Glu Arg Asp Met Ser		
	195	200	205
40	Leu Arg Leu Asn Glu Gln Tyr Glu His Ala Ser Ile His Leu Trp Asp		
	210	215	220
45	Leu Leu Glu Gly Lys Glu Lys Ser Val Cys Gly Thr Thr Tyr Lys Ala		
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50	Leu Lys Glu Ile Val Glu Arg Val Phe Gln Ser Asn Tyr Phe Asp Ser		
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260 265 270

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Ala Pro Thr Val Glu Asp Gln Val Ala Glu Ala Glu Pro Glu Pro Ala
275 280 285

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Glu Glu Tyr Thr Glu Gln Ser Glu Val Glu Ser Thr Glu Tyr Val Asn
290 295 300

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Arg Gln Phe Met Ala Glu Thr Gln Phe Ser Ser Gly Glu Lys Glu Gln
305 310 315 320

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Val Asp Glu Trp Thr Val Glu Thr Val Glu Val Val Asn Ser Leu Gln
325 330 335

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Gln Gln Pro Gln Ala Ala Ser Pro Ser Val Pro Glu Pro His Ser Leu
340 345 350

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Thr Pro Val Ala Gln Ala Asp Pro Leu Val Arg Arg Gln Arg Val Gln
355 360 365

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Asp Leu Met Ala Gln Met Gln Gly Pro Tyr Asn Phe Ile Gln Asp Ser
370 375 380

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Met Leu Asp Phe Glu Asn Gln Thr Leu Asp Pro Ala Ile Val Ser Ala
385 390 395 400

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Gln Pro Met Asn Pro Thr Gln Asn Met Asp Met Pro Gln Leu Val Cys
405 410 415

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Pro Pro Val His Ser Glu Ser Arg Leu Ala Gln Pro Asn Gln Val Pro

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420

425

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5 Val Gln Pro Glu Ala Thr Gln Val Pro Leu Val Ser Ser Thr Ser Glu
435 440 445

10 Gly Tyr Thr Ala Ser Gln Pro Leu Tyr Gln Pro Ser His Ala Thr Glu
450 455 460

15 Gln Arg Pro Gln Lys Glu Pro Ile Asp Gln Ile Gln Ala Thr Ile Ser
465 470 475 480

20 Leu Asn Thr Asp Gln Thr Thr Ala Ser Ser Ser Leu Pro Ala Ala Ser
485 490 495

25 Gln Pro Gln Val Phe Gln Ala Gly Thr Ser Lys Pro Leu His Ser Ser
500 505 510

30 Gly Ile Asn Val Asn Ala Ala Pro Phe Gln Ser Met Gln Thr Val Phe
515 520 525

35 Asn Met Asn Ala Pro Val Pro Pro Val Asn Glu Pro Glu Thr Leu Lys
530 535 540

40 Gln Gln Asn Gln Tyr Gln Ala Ser Tyr Asn Gln Ser Phe Ser Ser Gln
545 550 555 560

45 Pro His Gln Val Glu Gln Thr Asp Leu Gln Gln Glu Gln Leu Gln Thr
565 570 575

50 Val Val Gly Thr Tyr His Gly Ser Gln Asp Gln Pro His Gln Val Thr
580 585 590

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Gly Asn His Gln Gln Pro Pro Gln Gln Asn Thr Gly Phe Pro Arg Ser
595 600 605

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Ser Gln Pro Tyr Tyr Asn Ser Arg Gly Val Ser Arg Gly Gly Ser Arg
610 615 620

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Gly Ala Arg Gly Leu Met Asn Gly Tyr Arg Gly Pro Ala Asn Gly Phe
625 630 635 640

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Arg Gly Gly Tyr Asp Gly Tyr Arg Pro Ser Phe Ser Asn Thr Pro Asn
645 650 655

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Ser Gly Tyr Thr Gln Ser Gln Phe Ser Ala Pro Arg Asp Tyr Ser Gly
660 665 670

25

Tyr Gln Arg Asp Gly Tyr Gln Gln Asn Phe Lys Arg Gly Ser Gly Gln
675 680 685

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Ser Gly Pro Arg Gly Ala Pro Arg Gly Arg Gly Gly Pro Pro Arg Pro
690 695 700

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Asn Arg Gly Met Pro Gln Met Asn Thr Gln Gln Val Asn
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	Met Pro Ser Ala Thr Ser His Ser Gly Ser	
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10	ggc agc aag tcg tcc gga ccg cca ccg ccg tcg ggt tcc tcc ggg aat	159
	Gly Ser Lys Ser Ser Gly Pro Pro Pro Pro Ser Gly Ser Ser Gly Asn	
	15 20 25	
15	gag gcg ggg gcc ggg gcc gcc gcg ccg gct tcc caa cac ccc atg acc	207
	Glu Ala Gly Ala Gly Ala Ala Ala Pro Ala Ser Gln His Pro Met Thr	
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20	ggc acc ggg gct gtc cag acc gag gcc atg aag cag att ctc ggg gtg	255
	Gly Thr Gly Ala Val Gln Thr Glu Ala Met Lys Gln Ile Leu Gly Val	
	45 50 55	
25	atc gac aag aaa ctt cgg aac ctg gag aag aaa aag ggc aag ctt gat	303
	Ile Asp Lys Lys Leu Arg Asn Leu Glu Lys Lys Lys Gly Lys Leu Asp	
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30	gat tat cag gaa cga atg aac aaa ggg gaa agg ctt aat caa gat cag	351
	Asp Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg Leu Asn Gln Asp Gln	
	75 80 85 90	
35	ctg gat gcc gtg tct aag tac cag gaa gtc aca aat aac ttg gag ttt	399
	Leu Asp Ala Val Ser Lys Tyr Gln Glu Val Thr Asn Asn Leu Glu Phe	
	95 100 105	
40	gca aaa gaa tta cag agg agt ttc atg gca tta agc caa gat att cag	447
	Ala Lys Glu Leu Gln Arg Ser Phe Met Ala Leu Ser Gln Asp Ile Gln	
	110 115 120	
45	aaa aca ata aag aag aca gca cgt cgg gag cag ctt atg aga gag gaa	495
	Lys Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln Leu Met Arg Glu Glu	
	125 130 135	
50	gct gaa cag aaa cgt tta aaa aca gta ctt gag ctg cag tat gtt ttg	543
	Ala Glu Gln Lys Arg Leu Lys Thr Val Leu Glu Leu Gln Tyr Val Leu	
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	Asp Lys Leu Gly Asp Asp Glu Val Arg Thr Asp Leu Lys Gln Gly Leu																	
	155				160				165				170					
10	aat gga gtg cca ata ttg tct gaa gag gag ttg tcg ttg tta gat gag														639			
	Asn Gly Val Pro Ile Leu Ser Glu Glu Glu Leu Ser Leu Leu Asp Glu																	
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15	ttc tac aaa tta gca gac cct gaa cga gac atg agc ttg agg ttg aat														687			
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	Lys Glu Lys Pro Val Cys Gly Thr Thr Tyr Lys Ala Leu Lys Glu Ile																	
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	Val Glu Arg Val Phe Gln Ser Asn Tyr Phe Asp Ser Thr His Asn His																	
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	Gln Asn Gly Leu Cys Glu Glu Glu Glu Ala Ala Ser Ala Pro Thr Val																	
					255				260				265					
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	Glu Asp Gln Ala Ala Glu Ala Glu Pro Glu Pro Val Glu Glu Tyr Thr																	
					270				275				280					
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	Ala Glu Thr Gln Phe Ser Ser Gly Glu Lys Glu Gln Val Asp Asp Trp																	
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	Ala Ala Ser Pro Ser Val Pro Glu Pro His Ser Leu Thr Pro Val Ala	
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	Gln Ala Asp Pro Leu Val Arg Arg Gln Arg Val Gln Asp Leu Met Ala	
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	Gln Met Gln Gly Pro Tyr Asn Phe Ile Gln Asp Ser Met Leu Asp Phe	
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	gaa aac cag aca ctt gat cct gcc att gta tct gca cag ccg atg aat	1263
	Glu Asn Gln Thr Leu Asp Pro Ala Ile Val Ser Ala Gln Pro Met Asn	
	380 385 390	
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	cca gca cag aac atg gac ata ccc cag ctg gtt tgc cct cca gtt cat	1311
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	Ser Glu Ser Arg Leu Ala Gln Pro Asn Gln Val Ser Val Gln Pro Glu	
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	Ala Thr Gln Val Pro Leu Val Ser Ser Thr Ser Glu Gly Tyr Thr Ala	
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	aag gaa ccg att gat cag att cag gcg acg atc tct tta aat aca gac	1503
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	Tyr Gln Ala Ser Tyr Asn Gln Ser Phe Ser Ser Gln Pro His Gln Val				
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	Glu Gln Thr Glu Leu Gln Gln Glu Gln Leu Gln Thr Val Val Gly Thr				
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	Tyr His Gly Ser Gln Asp Gln Pro His Gln Val Thr Gly Asn His Gln				
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	Gln Pro Pro Gln Gln Asn Thr Gly Phe Pro Arg Ser Asn Gln Pro Tyr				
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45	ttg atg aat gga tac aga gga cct gct aat gga ttc aga gga gga tat				1983
	Leu Met Asn Gly Tyr Arg Gly Pro Ala Asn Gly Phe Arg Gly Gly Tyr				
		620	625	630	
50	gat ggt tac cgc cct tca ttc tct act aac act cca aac agt ggt tat				2031
	Asp Gly Tyr Arg Pro Ser Phe Ser Thr Asn Thr Pro Asn Ser Gly Tyr				
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	aca caa tct caa ttc agt gct ccc cgg gac tac tct ggc tat cag cgg	2079
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	Asp Gly Tyr Gln Gln Asn Phe Lys Arg Gly Ser Gly Gln Ser Gly Pro	
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	cgg gga gcc cca cga ggt cgt gga ggg ccc cca aga ccc aac aga ggg	2175
	Arg Gly Ala Pro Arg Gly Arg Gly Gly Pro Pro Arg Pro Asn Arg Gly	
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	atg ccg caa atg aac act cag caa gtg aat taa tctgattcac aggattatgt	2228
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35 40 45

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Thr Glu Ala Met Lys Gln Ile Leu Gly Val Ile Asp Lys Lys Leu Arg

50 55 60

Asn Leu Glu Lys Lys Lys Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met

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Asn Lys Gly Glu Arg Leu Asn Gln Asp Gln Leu Asp Ala Val Ser Lys
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Tyr Gln Glu Val Thr Asn Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg
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Ser Phe Met Ala Leu Ser Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr
115 120 125

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Ala Arg Arg Glu Gln Leu Met Arg Glu Glu Ala Glu Gln Lys Arg Leu
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Lys Thr Val Leu Glu Leu Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp
145 150 155 160

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Glu Val Arg Thr Asp Leu Lys Gln Gly Leu Asn Gly Val Pro Ile Leu
165 170 175

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Ser Glu Glu Glu Leu Ser Leu Leu Asp Glu Phe Tyr Lys Leu Ala Asp
180 185 190

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Pro Glu Arg Asp Met Ser Leu Arg Leu Asn Glu Gln Tyr Glu His Ala
195 200 205

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Ser Ile His Leu Trp Asp Leu Leu Glu Gly Lys Glu Lys Pro Val Cys
210 215 220

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Gly Thr Thr Tyr Lys Ala Leu Lys Glu Ile Val Glu Arg Val Phe Gln
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Ser Asn Tyr Phe Asp Ser Thr His Asn His Gln Asn Gly Leu Cys Glu
245 250 255

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	385					390					395					400	
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Gln Pro Asn Gln Val Ser Val Gln Pro Glu Ala Thr Gln Val Pro Leu
420 425 430

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Val Ser Ser Thr Ser Glu Gly Tyr Thr Ala Ser Gln Pro Leu Tyr Gln
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Pro Ser His Ala Thr Asp Gln Arg Pro Gln Lys Glu Pro Ile Asp Gln
450 455 460

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Ile Gln Ala Thr Ile Ser Leu Asn Thr Asp Gln Thr Thr Ala Ser Ser
465 470 475 480

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Ser Leu Pro Ala Ala Ser Gln Pro Gln Val Phe Gln Ala Gly Thr Ser
485 490 495

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Lys Pro Leu His Ser Ser Gly Ile Asn Val Asn Ala Ala Pro Phe Gln
500 505 510

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Ser Met Gln Thr Val Phe Asn Met Asn Ala Pro Val Pro Pro Val Asn
515 520 525

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Glu Pro Glu Thr Leu Lys Gln Gln Asn Gln Tyr Gln Ala Ser Tyr Asn
530 535 540

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Gln Ser Phe Ser Ser Gln Pro His Gln Val Glu Gln Thr Glu Leu Gln
545 550 555 560

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Gln Glu Gln Leu Gln Thr Val Val Gly Thr Tyr His Gly Ser Gln Asp
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Gln Pro His Gln Val Thr Gly Asn His Gln Gln Pro Pro Gln Gln Asn
580 585 590

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Thr Gly Phe Pro Arg Ser Asn Gln Pro Tyr Tyr Asn Ser Arg Gly Val
595 600 605

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Ser Arg Gly Gly Ser Arg Gly Ala Arg Gly Leu Met Asn Gly Tyr Arg
610 615 620

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Gly Pro Ala Asn Gly Phe Arg Gly Gly Tyr Asp Gly Tyr Arg Pro Ser
625 630 635 640

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Phe Ser Thr Asn Thr Pro Asn Ser Gly Tyr Thr Gln Ser Gln Phe Ser
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Ala Pro Arg Asp Tyr Ser Gly Tyr Gln Arg Asp Gly Tyr Gln Gln Asn
660 665 670

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Phe Lys Arg Gly Ser Gly Gln Ser Gly Pro Arg Gly Ala Pro Arg Gly
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	Arg Leu Asn Gln Asp Gln Leu Asp Ala Val Ser Lys Tyr Gln Glu Val	
	20 25 30	
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	Thr Asn Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg Ser Phe Met Ala	
	35 40 45	
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	Leu Ser Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr Ala Arg Arg Glu	
	50 55 60	
25	cag ctt atg aga gaa gaa gct gaa cag aaa cgt tta aaa act gta ctt	240
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	65 70 75 80	
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	Glu Leu Gln Tyr Val Leu Asp Lys Leu Gly Asp Glu Glu Val Arg Thr	
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	100 105 110	
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	130 135 140	
50	tgg gac ttg ctg gaa ggg aag gaa aaa tct gtc tgt gga aca acc tat	480
	Trp Asp Leu Leu Glu Gly Lys Glu Lys Ser Val Cys Gly Thr Thr Tyr	
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	Lys Ala Leu Arg Glu Ile Val Glu Arg Val Phe Gln Ser Asn Tyr Phe	
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	gac agc acc cac aac cac cag aat ggg ctc tgt gag gag gaa gag gct	576
	Asp Ser Thr His Asn His Gln Asn Gly Leu Cys Glu Glu Glu Glu Ala	
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	acc tca gct cca aca gct gaa gac cag gga gct gaa gct gaa cct gag	624
	Thr Ser Ala Pro Thr Ala Glu Asp Gln Gly Ala Glu Ala Glu Pro Glu	
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	cca gca gaa gaa tac act gaa caa agt gaa gtt gaa tca aca gag tat	672
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	Val Asn Arg Gln Phe Met Ala Glu Ala Gln Phe Ser Gly Glu Lys Glu	
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	Gln Val Asp Glu Trp Thr Val Glu Thr Val Glu Val Val Asn Ser Leu	
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	Gln Gln Gln Pro Gln Ala Ala Ser Pro Ser Val Pro Glu Pro His Ser	
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	Leu Thr Pro Val Ala Gln Ala Asp Pro Leu Val Arg Arg Gln Arg Val	
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	Gln Asp Leu Met Ala Gln Met Gln Gly Pro Tyr Asn Phe Ile Gln Asp	
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	370 375 380	
20	gag caa cga ccg caa aag gaa ccg act gac cag atc cag gca aca atc Glu Gln Arg Pro Gln Lys Glu Pro Thr Asp Gln Ile Gln Ala Thr Ile	1200
	385 390 395 400	
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	405 410 415	
30	tct cag cct cag gtg ttc cag gct ggg aca agc aaa cct tta cac agc Ser Gln Pro Gln Val Phe Gln Ala Gly Thr Ser Lys Pro Leu His Ser	1296
	420 425 430	
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	435 440 445	
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Val Asn Arg Gln Phe Met Ala Glu Ala Gln Phe Ser Gly Glu Lys Glu
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Gln Val Asp Glu Trp Thr Val Glu Thr Val Glu Val Val Asn Ser Leu
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Ala Gln Pro Met Asn Pro Ala Gln Asn Met Asp Met Pro Gln Leu Val

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45	Lys Gln Gln Asn Gln Tyr Gln Ala Ser Tyr Asn Gln Ser Phe Ser Ser		
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Thr Gly Asn His Gln Gln Pro Pro Gln Gln Asn Thr Gly Phe Pro Arg
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Ser Ser Gln Pro Tyr Tyr Asn Ser Arg Gly Val Ser Arg Gly Gly Ser
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Arg Gly Ala Arg Gly Leu Met Asn Gly Tyr Arg Gly Pro Ala Asn Gly
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Phe Arg Gly Gly Tyr Asp Gly Tyr Arg Pro Ser Phe Ser Asn Thr Pro
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Asn Ser Gly Tyr Thr Gln Ser Gln Phe Ser Ala Pro Arg Asp Tyr Ser
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Gly Tyr Gln Arg Asp Gly Tyr Gln Gln Asn Phe Lys Arg Gly Ser Gly
595 600 605

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	gct gcg ccg gct tct cag cat ccg gca acc ggc acc ggc gcc gtc cag	322
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55	Ser Phe Met Ala Leu Ser Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr	

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	gtt gta aac tca ctc cag cag caa cct cag gct gcg tcc cct tca gtc	1186
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Met Pro Gln Leu Val Cys Pro Gln Val His Ser Glu Ser Arg Leu Ala
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Val Ser Ser Thr Ser Glu Gly Tyr Thr Ala Ser Gln Pro Leu Tyr Gln
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Ile Gln Ala Thr Ile Ser Leu Asn Thr Asp Gln Thr Thr Ala Ser Ser
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Ser Leu Pro Ala Ala Ser Gln Pro Gln Val Phe Gln Ala Gly Thr Ser
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Lys Pro Leu His Ser Ser Gly Ile Asn Val Asn Ala Ala Pro Phe Gln
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Ser Met Gln Thr Val Phe Asn Met Asn Ala Pro Val Pro Pro Ala Asn
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Glu Pro Glu Thr Leu Lys Gln Gln Ser Gln Tyr Gln Ala Thr Tyr Asn
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20	Thr Gly Phe Pro Arg Ser Ser Gln Pro Tyr Tyr Asn Ser Arg Gly Val	595	600	605	
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tctctctcg gtctaaag atg ccc tcg gcc acc agc cac agc gga agc ggc 171
Met Pro Ser Ala Thr Ser His Ser Gly Ser Gly
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Ser Lys Ser Ser Gly Pro Pro Pro Pro Ser Gly Ser Ser Gly Ser Glu
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Ala Ala Ala Gly Ala Ala Ala Pro Ala Ser Gln His Pro Ala Thr Gly
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acc ggc gcc gtc cag acc gag gcc atg aag cag att ctc ggc gta atc 315
Thr Gly Ala Val Gln Thr Glu Ala Met Lys Gln Ile Leu Gly Val Ile
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gac aag aaa ctt cgg aac ctg gag aag aaa aag ggt aaa ctt gat gat 363
Asp Lys Lys Leu Arg Asn Leu Glu Lys Lys Lys Gly Lys Leu Asp Asp
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tac cag gaa cga atg aat aaa ggg gaa agg ctc aat caa gac cag ctg 411
Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg Leu Asn Gln Asp Gln Leu
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	Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln Leu Met Arg Glu Glu Ala	
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	Glu Gln Lys Arg Leu Lys Thr Val Leu Glu Leu Gln Tyr Val Leu Asp	
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	Glu Lys Pro Val Cys Gly Thr Thr Tyr Lys Ala Leu Lys Glu Ile Val	
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Ala Ala Pro Ala Ser Gln His Pro Ala Thr Gly Thr Gly Ala Val Gln
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Thr Glu Ala Met Lys Gln Ile Leu Gly Val Ile Asp Lys Lys Leu Arg
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Asn Leu Glu Lys Lys Lys Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met
65 70 75 80

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Asn Lys Gly Glu Arg Leu Asn Gln Asp Gln Leu Asp Ala Val Ser Lys
85 90 95

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Tyr Gln Glu Val Thr Asn Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg
100 105 110

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Ser Phe Met Ala Leu Ser Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr
115 120 125

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Ala Arg Arg Glu Gln Leu Met Arg Glu Glu Ala Glu Gln Lys Arg Leu
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Lys Thr Val Leu Glu Leu Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp
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Asp Val Arg Thr Asp Leu Lys Gln Gly Leu Ser Gly Val Pro Ile Leu

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15	Ser Ile His Leu Trp Asp Leu Leu Glu Gly Lys Glu Lys Pro Val Cys		
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20	Gly Thr Thr Tyr Lys Ala Leu Lys Glu Ile Val Glu Arg Val Phe Gln		
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25	Ser Asn Tyr Phe Asp Ser Thr His Asn His Gln Asn Gly Leu Cys Glu		
	245	250	255
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Pro Glu Pro His Ser Leu Thr Pro Val Ala Gln Ser Asp Pro Leu Val
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Arg Arg Gln Arg Val Gln Asp Leu Met Ala Gln Met Gln Gly Pro Tyr
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Pro Ala Ile Val Ser Ala Gln Pro Met Asn Pro Thr Gln Asn Met Asp
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Met Pro Gln Leu Val Cys Pro Gln Val His Ser Glu Ser Arg Leu Ala
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Gln Ser Asn Gln Val Pro Val Gln Pro Glu Ala Thr Gln Val Pro Leu
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Val Ser Ser Thr Ser Glu Gly Tyr Thr Ala Ser Gln Pro Leu Tyr Gln
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Pro Ser His Ala Thr Glu Gln Arg Pro Gln Lys Glu Pro Met Asp Gln
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Ile Gln Ala Thr Ile Ser Leu Asn Thr Asp Gln Thr Thr Ala Ser Ser
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Ser Leu Pro Ala Ala Ser Gln Pro Gln Val Phe Gln Ala Gly Thr Ser
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Lys Pro Leu His Ser Ser Gly Ile Asn Val Asn Ala Ala Pro Phe Gln

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Ser Met Gln Thr Val Phe Asn Met Asn Ala Pro Val Pro Pro Ala Asn
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Glu Pro Glu Thr Leu Lys Gln Gln Ser Gln Tyr Gln Ala Thr Tyr Asn
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Gln Ser Phe Ser Ser Gln Pro His Gln Val Glu Gln Thr Glu Leu Gln
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Gln Pro His Gln Val Pro Gly Asn His Gln Gln Pro Pro Gln Gln Asn
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Thr Gly Phe Pro Arg Ser Ser Gln Pro Tyr Tyr Asn Ser Arg Gly Val
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Ser Arg Gly Gly Ser Arg Gly Ala Arg Gly Leu Met Asn Gly Tyr Arg
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Gly Pro Ala Asn Gly Phe Arg Gly Gly Tyr Asp Gly Tyr Arg Pro Ser
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Phe Ser Asn Thr Pro Asn Ser Gly Tyr Ser Gln Ser Gln Phe Thr Ala
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Pro Arg Asp Tyr Ser Gly Tyr Gln Arg Asp Gly Tyr Gln Gln Asn Phe
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Gln Val Asn
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Ala Ala Ala Gly Ala Ala Ala Pro Ala Ser Gln His Pro Ala Thr Gly
30 35 40

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Thr Gly Ala Val Gln Thr Glu Ala Met Lys Gln Ile Leu Gly Val Ile

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50	atg caa ggg ccc tat aat ttc ata cag acg ctt gat cct gcc att gta Met Gln Gly Pro Tyr Asn Phe Ile Gln Thr Leu Asp Pro Ala Ile Val 365 370 375	1275
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10	gtt cct gta caa cca gaa gcc aca cag gtt cct ttg gtt tca tcc aca Val Pro Val Gln Pro Glu Ala Thr Gln Val Pro Leu Val Ser Ser Thr	415	420	425	1419
15	agt gag ggg tat aca gca tct cag ccc ttg tac cag cca tct cat gct Ser Glu Gly Tyr Thr Ala Ser Gln Pro Leu Tyr Gln Pro Ser His Ala	430	435	440	1467
20	acg gag cag cgg ccg cag aaa gag cca atg gat cag att cag gca aca Thr Glu Gln Arg Pro Gln Lys Glu Pro Met Asp Gln Ile Gln Ala Thr	445	450	455	1515
25	ata tct ttg aat aca gac cag act aca gca tcc tca tcc ctt cct gct Ile Ser Leu Asn Thr Asp Gln Thr Thr Ala Ser Ser Ser Leu Pro Ala	460	465	470	1563
30	gct tct cag cct caa gtg ttc cag gct ggg aca agt aaa cct ttg cac Ala Ser Gln Pro Gln Val Phe Gln Ala Gly Thr Ser Lys Pro Leu His	480	485	490	1611
35	agc agt gga atc aat gta aat gca gct cca ttc cag tcc atg caa acg Ser Ser Gly Ile Asn Val Asn Ala Ala Pro Phe Gln Ser Met Gln Thr	495	500	505	1659
40	gtg ttc aat atg aat gct cca gtc cct cct gct aat gaa cca gaa acg Val Phe Asn Met Asn Ala Pro Val Pro Pro Ala Asn Glu Pro Glu Thr	510	515	520	1707
45	tta aaa caa cag agt cag tac cag gcc act tat aac cag agt ttt tcc Leu Lys Gln Gln Ser Gln Tyr Gln Ala Thr Tyr Asn Gln Ser Phe Ser	525	530	535	1755
50	agt cag cct cac caa gtg gaa caa aca gag ctt caa caa gac caa ctg Ser Gln Pro His Gln Val Glu Gln Thr Glu Leu Gln Gln Asp Gln Leu	540	545	550	1803
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30	640 645 650	
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	ggg cag agt gga cca cgg gga gcc cca cga ggt cgt gga ggg ccc cca	2187
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40	670 675 680	
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Ala Ala Pro Ala Ser Gln His Pro Ala Thr Gly Thr Gly Ala Val Gln
 35 40 45

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Thr Glu Ala Met Lys Gln Ile Leu Gly Val Ile Asp Lys Lys Leu Arg
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Asn Leu Glu Lys Lys Lys Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met
 65 70 75 80

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Asn Lys Gly Glu Arg Leu Asn Gln Asp Gln Leu Asp Ala Val Ser Lys
 85 90 95

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Tyr Gln Glu Val Thr Asn Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg
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Ser Phe Met Ala Leu Ser Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr
 115 120 125

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Ala Arg Arg Glu Gln Leu Met Arg Glu Glu Ala Glu Gln Lys Arg Leu
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Lys Thr Val Leu Glu Leu Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp
145 150 155 160

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Asp Val Arg Thr Asp Leu Lys Gln Gly Leu Ser Gly Val Pro Ile Leu
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Ser Glu Glu Glu Leu Ser Leu Leu Asp Glu Phe Tyr Lys Leu Val Asp
180 185 190

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Pro Glu Arg Asp Met Ser Leu Arg Leu Asn Glu Gln Tyr Glu His Ala
195 200 205

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Ser Ile His Leu Trp Asp Leu Leu Glu Gly Lys Glu Lys Pro Val Cys
210 215 220

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Gly Thr Thr Tyr Lys Ala Leu Lys Glu Ile Val Glu Arg Val Phe Gln
225 230 235 240

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Ser Asn Tyr Phe Asp Ser Thr His Asn His Gln Asn Gly Leu Cys Glu
245 250 255

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Glu Glu Glu Ala Ala Ser Ala Pro Thr Val Glu Asp Gln Val Ala Glu
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Ser Thr Glu Tyr Val Asn Arg Gln Phe Met Ala Glu Thr Gln Phe Ser
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Ser Gly Glu Lys Glu Gln Val Asp Glu Trp Thr Val Glu Thr Val Glu
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	Arg Arg Gln Arg Val Gln Asp Leu Met Ala Gln Met Gln Gly Pro Tyr	
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	Asn Phe Ile Gln Thr Leu Asp Pro Ala Ile Val Ser Ala Gln Pro Met	
	370	375 380
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	Asn Pro Thr Gln Asn Met Asp Met Pro Gln Leu Val Cys Pro Gln Val	
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	His Ser Glu Ser Arg Leu Ala Gln Ser Asn Gln Val Pro Val Gln Pro	
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	Glu Ala Thr Gln Val Pro Leu Val Ser Ser Thr Ser Glu Gly Tyr Thr	
	420	425 430
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	Ala Ser Gln Pro Leu Tyr Gln Pro Ser His Ala Thr Glu Gln Arg Pro	
	435	440 445
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	Gln Lys Glu Pro Met Asp Gln Ile Gln Ala Thr Ile Ser Leu Asn Thr	
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	Asp Gln Thr Thr Ala Ser Ser Ser Leu Pro Ala Ala Ser Gln Pro Gln	
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Val Phe Gln Ala Gly Thr Ser Lys Pro Leu His Ser Ser Gly Ile Asn
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Val Asn Ala Ala Pro Phe Gln Ser Met Gln Thr Val Phe Asn Met Asn
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Ala Pro Val Pro Pro Ala Asn Glu Pro Glu Thr Leu Lys Gln Gln Ser
515 520 525

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Gln Tyr Gln Ala Thr Tyr Asn Gln Ser Phe Ser Ser Gln Pro His Gln
530 535 540

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Val Glu Gln Thr Glu Leu Gln Gln Asp Gln Leu Gln Thr Val Val Gly
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Thr Tyr His Gly Ser Gln Asp Gln Pro His Gln Val Pro Gly Asn His
565 570 575

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Gln Gln Pro Pro Gln Gln Asn Thr Gly Phe Pro Arg Ser Ser Gln Pro
580 585 590

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Tyr Tyr Asn Ser Arg Gly Val Ser Arg Gly Gly Ser Arg Gly Ala Arg
595 600 605

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Gly Leu Met Asn Gly Tyr Arg Gly Pro Ala Asn Gly Phe Arg Gly Gly
610 615 620

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Tyr Asp Gly Tyr Arg Pro Ser Phe Ser Asn Thr Pro Asn Ser Gly Tyr
625 630 635 640

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Ser Gln Ser Gln Phe Thr Ala Pro Arg Asp Tyr Ser Gly Tyr Gln Arg
645 650 655

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Asp Gly Tyr Gln Gln Asn Phe Lys Arg Gly Ser Gly Gln Ser Gly Pro
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atg ccc tcg gcc acc agc cac agc gga agc ggc agc aaa tcg tcg gga 226

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35 40 45

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15	aat aaa ggg gaa agg ctc aat caa gac cag ctg gat gcc gta tct aag Asn Lys Gly Glu Arg Leu Asn Gln Asp Gln Leu Asp Ala Val Ser Lys 85 90 95	466
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30	gca cgt cgg gaa cag ctt atg aga gaa gaa gca gaa cag aag cgc tta Ala Arg Arg Glu Gln Leu Met Arg Glu Glu Ala Glu Gln Lys Arg Leu 130 135 140	610
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	245 250 255	
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	Ala Glu Pro Glu Pro Ala Glu Glu Tyr Thr Glu Gln Ser Glu Val Glu	
	275 280 285	
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	Ser Thr Glu Tyr Val Asn Arg Gln Phe Met Ala Glu Thr Gln Phe Ser	
	290 295 300	
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	Ser Gly Glu Lys Glu Gln Val Asp Glu Trp Thr Val Glu Thr Val Glu	
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	Val Val Asn Ser Leu Gln Gln Gln Pro Gln Ala Ala Ser Pro Ser Val	
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	Pro Glu Pro His Ser Leu Thr Pro Val Ala Gln Ser Asp Pro Leu Val	
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	Asn Phe Ile Gln Asp Ser Met Leu Asp Phe Glu Asn Gln Thr Leu Asp	
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25	cca tct cat gct acg gag cag cgg ccg cag aaa gag cca atg gat cag Pro Ser His Ala Thr Glu Gln Arg Pro Gln Lys Glu Pro Met Asp Gln 450 455 460	1570
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	Gln Pro His Gln Val Pro Gly Asn His Gln Gln Pro Pro Gln Gln Asn			
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	Thr Gly Phe Pro Arg Ser Ser Gln Pro Tyr Tyr Asn Ser Arg Gly Val			
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	Ser Arg Gly Gly Ser Arg Gly Ala Arg Gly Leu Met Asn Gly Tyr Arg			
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	Gly Pro Ala Asn Gly Phe Arg Gly Gly Tyr Asp Gly Tyr Arg Pro Ser			
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	675	680	685	
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	Ile Leu Trp Trp			
	690			
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Thr Glu Ala Met Lys Gln Ile Leu Gly Val Ile Asp Lys Lys Leu Arg
25 50 55 60

Asn Leu Glu Lys Lys Lys Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met
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Asn Lys Gly Glu Arg Leu Asn Gln Asp Gln Leu Asp Ala Val Ser Lys
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Tyr Gln Glu Val Thr Asn Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg
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Ser Phe Met Ala Leu Ser Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr
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Ala Arg Arg Glu Gln Leu Met Arg Glu Glu Ala Glu Gln Lys Arg Leu
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Lys Thr Val Leu Glu Leu Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp
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	165	170	175
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Ser Glu Glu Glu Leu Ser Leu Leu Asp Glu Phe Tyr Lys Leu Val Asp			
	180	185	190
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Pro Glu Arg Asp Met Ser Leu Arg Leu Asn Glu Gln Tyr Glu His Ala			
	195	200	205
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Ser Ile His Leu Trp Asp Leu Leu Glu Gly Lys Glu Lys Pro Val Cys			
	210	215	220
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Gly Thr Thr Tyr Lys Ala Leu Lys Glu Ile Val Glu Arg Val Phe Gln			
225	230	235	240
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Ser Asn Tyr Phe Asp Ser Thr His Asn His Gln Asn Gly Leu Cys Glu			
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Glu Glu Glu Ala Ala Ser Ala Pro Thr Val Glu Asp Gln Val Ala Glu			
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Ser Gly Glu Lys Glu Gln Val Asp Glu Trp Thr Val Glu Thr Val Glu			
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Val Val Asn Ser Leu Gln Gln Gln Pro Gln Ala Ala Ser Pro Ser Val
325 330 335

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Pro Glu Pro His Ser Leu Thr Pro Val Ala Gln Ser Asp Pro Leu Val
340 345 350

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Arg Arg Gln Arg Val Gln Asp Leu Met Ala Gln Met Gln Gly Pro Tyr
355 360 365

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Asn Phe Ile Gln Asp Ser Met Leu Asp Phe Glu Asn Gln Thr Leu Asp
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Pro Ala Ile Val Ser Ala Gln Pro Met Asn Pro Thr Gln Asn Met Asp
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Met Pro Gln Leu Val Cys Pro Gln Val His Ser Glu Ser Arg Leu Ala
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Gln Ser Asn Gln Val Pro Val Gln Pro Glu Ala Thr Gln Val Pro Leu
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Val Ser Ser Thr Ser Glu Gly Tyr Thr Ala Ser Gln Pro Leu Tyr Gln
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Pro Ser His Ala Thr Glu Gln Arg Pro Gln Lys Glu Pro Met Asp Gln
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Ser Leu Pro Ala Ala Ser Gln Pro Gln Val Phe Gln Ala Gly Thr Ser

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485

490

495

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20 Gln Ser Phe Ser Ser Gln Pro His Gln Val Glu Gln Thr Glu Leu Gln
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25 Gln Asp Gln Leu Gln Thr Val Val Gly Thr Tyr His Gly Ser Gln Asp
565 570 575

30 Gln Pro His Gln Val Pro Gly Asn His Gln Gln Pro Pro Gln Gln Asn
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35 Thr Gly Phe Pro Arg Ser Ser Gln Pro Tyr Tyr Asn Ser Arg Gly Val
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40 Ser Arg Gly Gly Ser Arg Gly Ala Arg Gly Leu Met Asn Gly Tyr Arg
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45 Gly Pro Ala Asn Gly Phe Arg Gly Gly Tyr Asp Gly Tyr Arg Pro Ser
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50 Phe Ser Asn Thr Pro Asn Ser Gly Tyr Ser Gln Ser Gln Phe Thr Ala
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Pro Arg Asp Tyr Ser Gly Tyr Gln Arg Asp Gly Tyr Gln Gln Asn Phe
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Met Pro Ser Ala Thr Ser His Ser Gly Ser Gly
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agc aaa tgc tgc gga ccg ccg ccg tcc ggt tcc tcc ggg agt gag 219
Ser Lys Ser Ser Gly Pro Pro Pro Pro Ser Gly Ser Ser Gly Ser Glu
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30 35 40

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acc ggc gcc gtc cag acc gag gcc atg aag cag att ctc ggc gta atc 315
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20	aag gaa tta cag agg agt ttc atg gca tta agt caa gat att cag aaa Lys Glu Leu Gln Arg Ser Phe Met Ala Leu Ser Gln Asp Ile Gln Lys 110 115 120				507
25	aca ata aag aag aca gca cgt cgg gaa cag ctt atg aga gaa gaa gca Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln Leu Met Arg Glu Glu Ala 125 130 135				555
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	Thr Thr Ala Ser Ser Ser Leu Pro Ala Ala Ser Gln Pro Gln Val Phe							
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	Gly Tyr Arg Pro Ser Phe Ser Asn Thr Pro Asn Ser Gly Tyr Ser Gln	
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Thr Glu Ala Met Lys Gln Ile Leu Gly Val Ile Asp Lys Lys Leu Arg
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Asn Leu Glu Lys Lys Lys Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met
65 70 75 80

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Asn Lys Gly Glu Arg Leu Asn Gln Asp Gln Leu Asp Ala Val Ser Lys
85 90 95

35

Tyr Gln Glu Val Thr Asn Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg
100 105 110

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Ser Phe Met Ala Leu Ser Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr
115 120 125

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Ala Arg Arg Glu Gln Leu Met Arg Glu Glu Ala Glu Gln Lys Arg Leu
130 135 140

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Lys Thr Val Leu Glu Leu Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp
145 150 155 160

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10	Ser Glu Glu Glu Leu Ser Leu Leu Asp Glu Phe Tyr Lys Leu Val Asp	180	185	190	
15	Pro Glu Arg Asp Met Ser Leu Arg Leu Asn Glu Gln Tyr Glu His Ala	195	200	205	
20	Ser Ile His Leu Trp Asp Leu Leu Glu Gly Lys Glu Lys Pro Val Cys	210	215	220	
25	Gly Thr Thr Tyr Lys Ala Leu Lys Glu Ile Val Glu Arg Val Phe Gln	225	230	235	240
30	Ser Asn Tyr Phe Asp Ser Thr His Asn His Gln Asn Gly Leu Cys Glu	245	250	255	
35	Glu Glu Glu Ala Ala Ser Ala Pro Thr Val Glu Asp Gln Val Ala Glu	260	265	270	
40	Ala Glu Pro Glu Pro Ala Glu Glu Tyr Thr Glu Gln Ser Glu Val Glu	275	280	285	
45	Ser Thr Glu Tyr Val Asn Arg Gln Phe Met Ala Glu Thr Gln Phe Ser	290	295	300	
50	Ser Gly Glu Lys Glu Gln Val Asp Glu Trp Thr Val Glu Thr Val Glu	305	310	315	320

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Val Val Asn Ser Leu Gln Gln Gln Pro Gln Ala Ala Ser Pro Ser Val
325 330 335

5

Pro Glu Pro His Ser Leu Thr Pro Val Ala Gln Ser Asp Pro Leu Val
340 345 350

10

Arg Arg Gln Arg Val Gln Asp Leu Met Ala Gln Met Gln Gly Pro Tyr
355 360 365

15

Asn Phe Ile Gln Asp Ser Met Leu Asp Phe Glu Asn Gln Thr Leu Asp
370 375 380

20

Pro Ala Ile Val Ser Ala Gln Pro Met Asn Pro Thr Gln Asn Met Asp
385 390 395 400

25

Met Pro Gln Leu Val Cys Pro Gln Val His Ser Glu Ser Arg Leu Ala
405 410 415

30

Gln Ser Asn Gln Val Pro Val Gln Pro Glu Ala Thr Gln Val Pro Leu
420 425 430

35

Val Ser Ser Thr Ser Glu Gly Tyr Thr Ala Ser Gln Pro Leu Tyr Gln
435 440 445

40

Pro Ser His Ala Thr Glu Gln Arg Pro Gln Lys Glu Pro Met Asp Gln
450 455 460

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Ile Gln Ala Thr Ile Ser Leu Asn Thr Asp Gln Thr Thr Ala Ser Ser
465 470 475 480

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Ser Leu Pro Ala Ala Ser Gln Pro Gln Val Phe Gln Ala Gly Thr Ser
485 490 495

55

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Lys Pro Leu His Ser Ser Gly Ile Asn Val Asn Ala Ala Pro Phe Gln
500 505 510

5

Ser Met Gln Thr Val Phe Asn Met Asn Ala Pro Val Pro Pro Ala Asn
515 520 525

10

Glu Pro Glu Thr Leu Lys Gln Gln Ser Gln Tyr Gln Ala Thr Tyr Asn
530 535 540

15

Gln Ser Phe Ser Ser Gln Pro His Gln Val Glu Gln Thr Glu Leu Gln
545 550 555 560

20

Gln Asp Gln Leu Gln Thr Val Val Gly Thr Tyr His Gly Ser Gln Asp
565 570 575

25

Gln Pro His Gln Val Pro Gly Asn His Gln Gln Pro Pro Gln Gln Asn
580 585 590

30

Thr Gly Phe Pro Arg Ser Ser Gln Pro Tyr Tyr Asn Ser Arg Gly Val
595 600 605

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Ser Arg Gly Gly Ser Arg Gly Ala Arg Gly Leu Met Asn Gly Tyr Arg
610 615 620

40

Gly Pro Ala Asn Gly Phe Arg Gly Gly Tyr Asp Gly Tyr Arg Pro Ser
625 630 635 640

45

Phe Ser Asn Thr Pro Asn Ser Gly Tyr Ser Gln Ser Gln Phe Thr Ala
645 650 655

50

55

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Pro Arg Asp Tyr Ser Gly Tyr Gln Arg Asp Gly Tyr Gln Gln Asn Phe
660 665 670

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Lys Arg Gly Ser Gly Gln Ser Gly Pro Arg Gly Ala Pro Arg Gly Asn
675 680 685

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Ile Leu Trp Trp
690

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<210> 29
<211> 2109
<212> DNA
<213> Gallus gallus

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<220>
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<222> (1).. (2109)
<223>

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<400> 29
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1 5 10 15

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ggc ccg ggc ggc aac gag cag gcc ccg gcg gcg gca gcg gcg gcc ccg 96
Gly Pro Gly Gly Asn Glu Gln Ala Pro Ala Ala Ala Ala Ala Pro
20 25 30

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cag gcg tcg ggc ggc agc atc acc tcg gtt cag acc gag gcc atg aag 144
Gln Ala Ser Gly Gly Ser Ile Thr Ser Val Gln Thr Glu Ala Met Lys
35 40 45

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cag atc ttg gga gtg atc gac aaa aag ctc cgc aac ctc gag aag aaa 192
Gln Ile Leu Gly Val Ile Asp Lys Lys Leu Arg Asn Leu Glu Lys Lys
50 55 60

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aag agc aaa ctt gac gat tac cag gaa cga atg aac aag ggg gaa cgt 240
Lys Ser Lys Leu Asp Asp Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg
65 70 75 80

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	cta aat caa gat caa ctg gat gca gtg tca aaa tac cag gaa gtg aca	288
	Leu Asn Gln Asp Gln Leu Asp Ala Val Ser Lys Tyr Gln Glu Val Thr	
5	85 90 95	
	aat aac ctg gaa ttc gct aaa gaa ctg cag agg agc ttt atg gca ctg	336
	Asn Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg Ser Phe Met Ala Leu	
10	100 105 110	
	agc caa gat atc cag aaa aca ata aaa aag acg gct cgc agg gag cag	384
	Ser Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln	
15	115 120 125	
	ctg atg aga gaa gag gct gag cag aag cgt tta aag act gtg cta gag	432
	Leu Met Arg Glu Glu Ala Glu Gln Lys Arg Leu Lys Thr Val Leu Glu	
20	130 135 140	
	ctg cag ttc att ttg gac aag ttg ggt gac gat gaa gtg cgc agt gac	480
	Leu Gln Phe Ile Leu Asp Lys Leu Gly Asp Asp Glu Val Arg Ser Asp	
25	145 150 155 160	
	ttg aaa caa gga tca aat gga gta ccg gta ctg aca gag gag gaa ctg	528
	Leu Lys Gln Gly Ser Asn Gly Val Pro Val Leu Thr Glu Glu Glu Leu	
30	165 170 175	
	aca atg ctg gat gaa ttt tac aag cta gtt tac cct gaa agg gac atg	576
	Thr Met Leu Asp Glu Phe Tyr Lys Leu Val Tyr Pro Glu Arg Asp Met	
35	180 185 190	
	aac atg agg ttg aat gag cag tat gag caa gca tct gtt cac ctg tgg	624
	Asn Met Arg Leu Asn Glu Gln Tyr Glu Gln Ala Ser Val His Leu Trp	
40	195 200 205	
	gac tta ctg gaa ggg aag gaa aaa ccc gtt tgt gga aca acc tat aaa	672
	Asp Leu Leu Glu Gly Lys Glu Lys Pro Val Cys Gly Thr Thr Tyr Lys	
45	210 215 220	
	gcc ctg aag gag gtt gtt gaa cgt att ctt caa act agt tac ttt gat	720
	Ala Leu Lys Glu Val Val Glu Arg Ile Leu Gln Thr Ser Tyr Phe Asp	
50	225 230 235 240	
	agc acc cat aac cat cag aac ggg tta tgt gag gaa gaa gag gca gca	768
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	Ser Thr His Asn His Gln Asn Gly Leu Cys Glu Glu Glu Glu Ala Ala	
	245 250 255	
5	ccc aca cct gca gta gaa gac act gta gca gaa gct gag cct gat cca Pro Thr Pro Ala Val Glu Asp Thr Val Ala Glu Ala Glu Pro Asp Pro	816
	260 265 270	
10	gca gaa gaa ttt act gaa cct act gaa gtt gaa tcg act gag tat gta Ala Glu Glu Phe Thr Glu Pro Thr Glu Val Glu Ser Thr Glu Tyr Val	864
	275 280 285	
15	aac aga caa ttc atg gca gag act cag ttc agc agt agt gag aag gaa Asn Arg Gln Phe Met Ala Glu Thr Gln Phe Ser Ser Ser Glu Lys Glu	912
	290 295 300	
20	cag gta gat gag tgg aca gtt gaa acg gtt gag gtt gta aat tca ctg Gln Val Asp Glu Trp Thr Val Glu Thr Val Glu Val Val Asn Ser Leu	960
	305 310 315 320	
25	cag caa caa aca caa gct aca tct cct cca gtt cct gaa cct cat aca Gln Gln Gln Thr Gln Ala Thr Ser Pro Pro Val Pro Glu Pro His Thr	1008
	325 330 335	
30	ctc act act gtg gct caa gca gat cct ctt gtt aga aga cag aga gta Leu Thr Thr Val Ala Gln Ala Asp Pro Leu Val Arg Arg Gln Arg Val	1056
	340 345 350	
35	cag gac ctt atg gcc cag atg cag ggt cca tat aac ttc atg cag gac Gln Asp Leu Met Ala Gln Met Gln Gly Pro Tyr Asn Phe Met Gln Asp	1104
	355 360 365	
40	tct atg ctg gag ttt gag aac cag aca ctt gat cct gcc att gta tct Ser Met Leu Glu Phe Glu Asn Gln Thr Leu Asp Pro Ala Ile Val Ser	1152
	370 375 380	
45	gca cag ccc atg aat cca gca cag aat ttg gac atg ccg caa atg gtc Ala Gln Pro Met Asn Pro Ala Gln Asn Leu Asp Met Pro Gln Met Val	1200
	385 390 395 400	
50	tgc cct cca gtt cat act gag tca aga ctt gcc cag cct aat caa gtt Cys Pro Pro Val His Thr Glu Ser Arg Leu Ala Gln Pro Asn Gln Val	1248
	405 410 415	
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5	cct gtg caa cca gaa gct acg cag gtt ccc ttg gtt tca tct aca agt Pro Val Gln Pro Glu Ala Thr Gln Val Pro Leu Val Ser Ser Thr Ser	1296
	420 425 430	
10	gag gga tat aca gcc tcc cag ccc atg tat cag cct tct cat acc aca Glu Gly Tyr Thr Ala Ser Gln Pro Met Tyr Gln Pro Ser His Thr Thr	1344
	435 440 445	
15	gag caa cgg cca cag aag gaa tcc att gac cag att cag gct tca atg Glu Gln Arg Pro Gln Lys Glu Ser Ile Asp Gln Ile Gln Ala Ser Met	1392
	450 455 460	
20	tca ctg aat gca gac cag acc ccg tca tca tca tca ctt ccc act gca Ser Leu Asn Ala Asp Gln Thr Pro Ser Ser Ser Ser Leu Pro Thr Ala	1440
	465 470 475 480	
25	tcc cag ccg caa gtt ttc caa gct gga tct agc aaa cct ttg cat agc Ser Gln Pro Gln Val Phe Gln Ala Gly Ser Ser Lys Pro Leu His Ser	1488
	485 490 495	
30	agc gga atc aat gtt aat gca gct cca ttc caa tcc atg caa aca gta Ser Gly Ile Asn Val Asn Ala Ala Pro Phe Gln Ser Met Gln Thr Val	1536
	500 505 510	
35	ttc aac atg aat gca cct gtt cct cct gtt aat gag cca gaa gcc ctt Phe Asn Met Asn Ala Pro Val Pro Pro Val Asn Glu Pro Glu Ala Leu	1584
	515 520 525	
40	aag caa caa aat cag tac cag gcc agt tac aac cag agt ttc tcc aat Lys Gln Gln Asn Gln Tyr Gln Ala Ser Tyr Asn Gln Ser Phe Ser Asn	1632
	530 535 540	
45	cag cca cac caa gta gaa caa tca gat ctt cag caa gaa cag ctc cag Gln Pro His Gln Val Glu Gln Ser Asp Leu Gln Gln Glu Gln Leu Gln	1680
	545 550 555 560	
50	aca gtg gtt ggt act tac cat ggt tct ccg gac cag acc cat caa gtg Thr Val Val Gly Thr Tyr His Gly Ser Pro Asp Gln Thr His Gln Val	1728
	565 570 575	
55	gca gga aac cac cag caa cct ccc cag cag aat act gga ttt cca cgc	1776

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	Ala Gly Asn His Gln Gln Pro Pro Gln Gln Asn Thr Gly Phe Pro Arg	
	580 585 590	
5	aac agt cag cct tat tac aac agt cgg gga gtg tct cgt ggt gga tca	1824
	Asn Ser Gln Pro Tyr Tyr Asn Ser Arg Gly Val Ser Arg Gly Gly Ser	
	595 600 605	
10	cgt ggg act cgt gga ttg atg aat ggt tac agg gga cct gca aat gga	1872
	Arg Gly Thr Arg Gly Leu Met Asn Gly Tyr Arg Gly Pro Ala Asn Gly	
	610 615 620	
15	ttt aga gga gga tat gat ggc tac cgt cct tca ttt tcc aac act ccg	1920
	Phe Arg Gly Gly Tyr Asp Gly Tyr Arg Pro Ser Phe Ser Asn Thr Pro	
20	625 630 635 640	
	aac agt ggt tac acg cag ccc caa ttt aat gct cct cga gat tat tca	1968
	Asn Ser Gly Tyr Thr Gln Pro Gln Phe Asn Ala Pro Arg Asp Tyr Ser	
25	645 650 655	
	aac tac cag cgg gat gga tat cag cag aac ttc aaa cgt ggt tct gga	2016
	Asn Tyr Gln Arg Asp Gly Tyr Gln Gln Asn Phe Lys Arg Gly Ser Gly	
30	660 665 670	
	caa agt ggg cct cgg gga get cct cga ggt cgt gga ggg ccc cca aga	2064
	Gln Ser Gly Pro Arg Gly Ala Pro Arg Gly Arg Gly Gly Pro Pro Arg	
35	675 680 685	
	cca aac aga ggg atg cct caa atg aac gct cag caa gtg aat taa	2109
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	690 695 700	
45	<210> 30	
	<211> 702	
	<212> PRT	
50	<213> Gallus gallus	
	<400> 30	
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	1 5 10 15	

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Gly Pro Gly Gly Asn Glu Gln Ala Pro Ala Ala Ala Ala Ala Pro
20 25 30

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Gln Ala Ser Gly Gly Ser Ile Thr Ser Val Gln Thr Glu Ala Met Lys
35 40 45

10

Gln Ile Leu Gly Val Ile Asp Lys Lys Leu Arg Asn Leu Glu Lys Lys
50 55 60

15

Lys Ser Lys Leu Asp Asp Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg
65 70 75 80

20

Leu Asn Gln Asp Gln Leu Asp Ala Val Ser Lys Tyr Gln Glu Val Thr
85 90 95

25

Asn Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg Ser Phe Met Ala Leu
100 105 110

30

Ser Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln
115 120 125

35

Leu Met Arg Glu Glu Ala Glu Gln Lys Arg Leu Lys Thr Val Leu Glu
130 135 140

40

Leu Gln Phe Ile Leu Asp Lys Leu Gly Asp Asp Glu Val Arg Ser Asp
145 150 155 160

45

Leu Lys Gln Gly Ser Asn Gly Val Pro Val Leu Thr Glu Glu Glu Leu
165 170 175

50

Thr Met Leu Asp Glu Phe Tyr Lys Leu Val Tyr Pro Glu Arg Asp Met

55

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	180	185	190
5	Asn Met Arg Leu Asn Glu Gln Tyr Glu Gln Ala Ser Val His Leu Trp		
	195	200	205
10	Asp Leu Leu Glu Gly Lys Glu Lys Pro Val Cys Gly Thr Thr Tyr Lys		
	210	215	220
15	Ala Leu Lys Glu Val Val Glu Arg Ile Leu Gln Thr Ser Tyr Phe Asp		
	225	230	235
20	Ser Thr His Asn His Gln Asn Gly Leu Cys Glu Glu Glu Glu Ala Ala		
	245	250	255
25	Pro Thr Pro Ala Val Glu Asp Thr Val Ala Glu Ala Glu Pro Asp Pro		
	260	265	270
30	Ala Glu Glu Phe Thr Glu Pro Thr Glu Val Glu Ser Thr Glu Tyr Val		
	275	280	285
35	Asn Arg Gln Phe Met Ala Glu Thr Gln Phe Ser Ser Ser Glu Lys Glu		
	290	295	300
40	Gln Val Asp Glu Trp Thr Val Glu Thr Val Glu Val Val Asn Ser Leu		
	305	310	315
45	Gln Gln Gln Thr Gln Ala Thr Ser Pro Pro Val Pro Glu Pro His Thr		
	325	330	335
50	Leu Thr Thr Val Ala Gln Ala Asp Pro Leu Val Arg Arg Gln Arg Val		
	340	345	350

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Gln Asp Leu Met Ala Gln Met Gln Gly Pro Tyr Asn Phe Met Gln Asp
355 360 365

5

Ser Met Leu Glu Phe Glu Asn Gln Thr Leu Asp Pro Ala Ile Val Ser
370 375 380

10

Ala Gln Pro Met Asn Pro Ala Gln Asn Leu Asp Met Pro Gln Met Val
385 390 395 400

15

Cys Pro Pro Val His Thr Glu Ser Arg Leu Ala Gln Pro Asn Gln Val
405 410 415

20

Pro Val Gln Pro Glu Ala Thr Gln Val Pro Leu Val Ser Ser Thr Ser
420 425 430

25

Glu Gly Tyr Thr Ala Ser Gln Pro Met Tyr Gln Pro Ser His Thr Thr
435 440 445

30

Glu Gln Arg Pro Gln Lys Glu Ser Ile Asp Gln Ile Gln Ala Ser Met
450 455 460

35

Ser Leu Asn Ala Asp Gln Thr Pro Ser Ser Ser Ser Leu Pro Thr Ala
465 470 475 480

40

Ser Gln Pro Gln Val Phe Gln Ala Gly Ser Ser Lys Pro Leu His Ser
485 490 495

45

Ser Gly Ile Asn Val Asn Ala Ala Pro Phe Gln Ser Met Gln Thr Val
500 505 510

50

Phe Asn Met Asn Ala Pro Val Pro Pro Val Asn Glu Pro Glu Ala Leu

55

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515

520

525

5 Lys Gln Gln Asn Gln Tyr Gln Ala Ser Tyr Asn Gln Ser Phe Ser Asn
530 535 540

10 Gln Pro His Gln Val Glu Gln Ser Asp Leu Gln Gln Glu Gln Leu Gln
545 550 555 560

15 Thr Val Val Gly Thr Tyr His Gly Ser Pro Asp Gln Thr His Gln Val
565 570 575

20 Ala Gly Asn His Gln Gln Pro Pro Gln Gln Asn Thr Gly Phe Pro Arg
580 585 590

25 Asn Ser Gln Pro Tyr Tyr Asn Ser Arg Gly Val Ser Arg Gly Gly Ser
595 600 605

30 Arg Gly Thr Arg Gly Leu Met Asn Gly Tyr Arg Gly Pro Ala Asn Gly
610 615 620

35 Phe Arg Gly Gly Tyr Asp Gly Tyr Arg Pro Ser Phe Ser Asn Thr Pro
625 630 635 640

40 Asn Ser Gly Tyr Thr Gln Pro Gln Phe Asn Ala Pro Arg Asp Tyr Ser
645 650 655

45 Asn Tyr Gln Arg Asp Gly Tyr Gln Gln Asn Phe Lys Arg Gly Ser Gly
660 665 670

50 Gln Ser Gly Pro Arg Gly Ala Pro Arg Gly Arg Gly Gly Pro Pro Arg
675 680 685

Pro Asn Arg Gly Met Pro Gln Met Asn Ala Gln Gln Val Asn
690 695 700

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<213> Artificial

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<220>
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<210> 32
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<220>
<223> T7 primer

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<400> 32
taatacgact cactatagg

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<210> 33
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<220>
<223> primer

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<400> 33
aaggtttgaa tggagtgc

18

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<210> 34

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 <211> 18
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 <220>
 <223> primer

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 <400> 34
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 <210> 35
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 <212> DNA
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 catatggcat taagtcaaga tattcag 27

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<210> 38
 <211> 23
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<220>
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<400> 38
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<210> 39
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<220>
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<400> 39
 catatgccgt cggccaccag c 21

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<220>
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<400> 40
 ggtaccattc acttgctgag tg 22

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<210> 41

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<211> 23
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<220>
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<400> 41
 gagctcatgc cctcgccac cag

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<210> 42
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<220>
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<210> 43
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 <213> Homo sapiens

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<400> 43

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Arg Asn Leu Glu Lys Lys Lys Gly Lys Leu Asp Asp Tyr Gln
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<210> 44
 <211> 148
 <212> PRT
 <213> Mus musculus

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<400> 44

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Met Glu Trp Ser Gly Val Phe Ile Phe Leu Leu Ser Gly Thr Ala Gly

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	20	25	30
10	Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe		
	35	40	45
15	Thr Asp Tyr Asn Met Asp Trp Val Lys Gln Ser His Gly Lys Ser Leu		
	50	55	60
20	Glu Trp Ile Gly Asp Ile Asn Pro Asn Tyr Asp Ser Thr Ser Tyr Asn		
	65	70	75
25	Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser		
	85	90	95
30	Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Thr Ala Val		
	100	105	110
35	Tyr Tyr Cys Ala Arg Ser Arg Ser Tyr Asp Tyr Glu Gly Phe Ala Tyr		
	115	120	125
40	Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro		
	130	135	140
45	Pro Ser Val Tyr		
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55	<210> 45		
	<211> 132		
	<212> PRT		

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<213> Mus musculus

<400> 45

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Ala Val Leu Arg Cys Ser Arg Gly Leu Leu Val Ile Trp Ile Ser Asp
1 5 10 15

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Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Thr Ala Gly Glu
20 25 30

15

Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Trp Ser Val
35 40 45

20

Asn Gln Lys Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Gln Arg Gln Pro
50 55 60

25

Pro Lys Leu Leu Ile Tyr Gly Ala Ser Ile Arg Glu Ser Trp Val Pro
65 70 75 80

30

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

35

Ser Asn Val His Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln His Asn
100 105 110

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His Gly Ser Phe Leu Pro Ser Arg Ser Glu Gln Val Pro Ser Trp Arg
115 120 125

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Ser Asn Asn Arg
130

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<210> 46

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<211> 117

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<212> PRT

<213> Mus musculus

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<400> 46

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Arg Thr Thr Ser His Met Asp Ser Asp Ile Gln Leu Thr Gln Ser Pro
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Ala Ser Leu Ser Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg
20 25 30

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Ala Ser Gly Asn Ile His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Gln
35 40 45

25

Gly Lys Ser Pro Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Ala Asp
50 55 60

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Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser
65 70 75 80

35

Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp Phe Gly Ser Tyr Tyr Cys
85 90 95

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Gln His Phe Trp Ser Thr Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu
100 105 110

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Ile Lys Gln Ser Asp
115

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<210> 47

<211> 94

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<212> PRT

<213> Mus musculus

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<400> 47

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1 5 10 15

10 Asn Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu
20 25 30

15 Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe
35 40 45

20 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val
50 55 60

25 Glu Thr Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn Ser Trp
65 70 75 80

30 Pro Tyr Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Gln
85 90

35 <210> 48

<211> 105

<212> PRT

40 <213> Mus musculus

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45 Gly Leu Phe Cys Ser Val Glu Arg Cys His Tyr Gln Leu Gln Ser Ser
1 5 10 15

50 Gln Asn Leu Leu Ser Ile Val Asn Arg Tyr His Tyr Met Ser Gly Asn
20 25 30

55 Pro Pro Lys Leu Leu Val Tyr Pro Ala Leu Leu Ile Tyr Glu Ala Ser

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35

40

45

5 Ile Thr Lys Ser Cys Val Pro Asp Arg Phe Thr Arg Ser Gly Ser Gly
50 55 60

10 Thr Asn Phe Thr Leu Thr Ile Asn Phe Val His Ala Asp Asp Leu Ile
65 70 75 80

15 Phe Tyr Tyr Cys Gln His Asn Arg Gly Ser Phe Leu Pro Ser Ser Ser
85 90 95

20 Val Gln Val Pro Arg Arg Arg Ser Asn
100 105

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<210> 49
<211> 100
<212> PRT
<213> Mus musculus

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<400> 49

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Asp Ile Leu Gln Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn
1 5 10 15

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Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Ile Gly Leu Ile
20 25 30

45

Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys
35 40 45

50

Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu
50 55 60

55

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Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Trp
65 70 75 80

5

Gly Val Trp Ser Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
85 90 95

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Val Ser Ser Lys
100

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<210> 50
<211> 90
<212> PRT
<213> Mus musculus

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<400> 50

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Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Arg Thr Ala
1 5 10 15

30

Val Ala Trp Tyr Gln Gln Lys Pro Arg Gln Ser Pro Lys Ala Leu Ile
20 25 30

35

Tyr Leu Ala Ser Asn Arg Asp Thr Gly Leu Pro Asp Arg Phe Pro Gly
35 40 45

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Arg Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile Thr Asn Val Gln Ser
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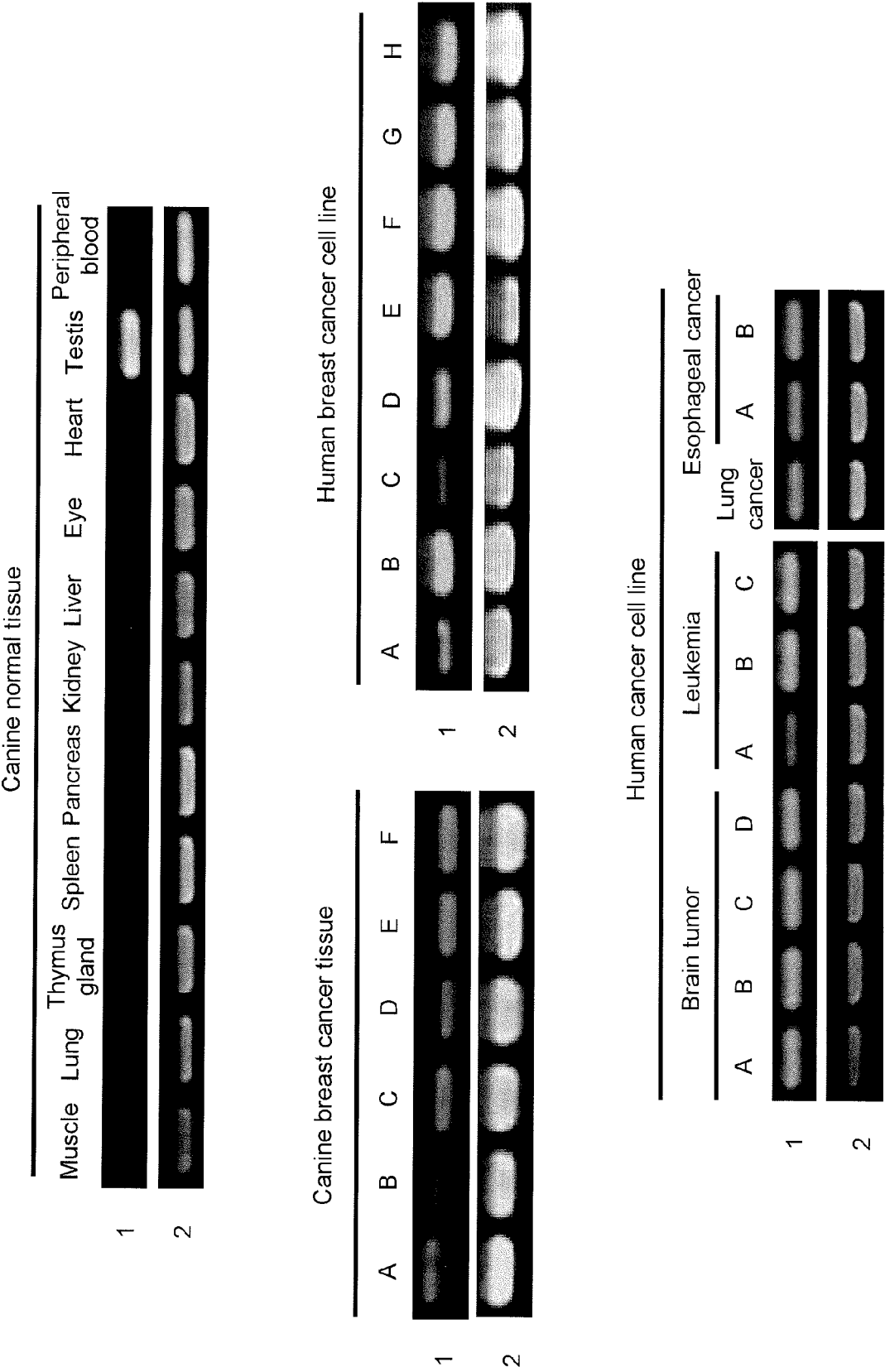
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Claims

1. A method for detecting a cancer, comprising measuring the expression of a polypeptide having a reactivity of binding via an antigen-antibody reaction to an antibody against a CAPRIN-1 protein having any one of the amino acid sequences shown in the even-numbered SEQ ID NOS: 2-30 in the Sequence Listing, in a sample separated from a living organism,
 wherein the cancer is at least one type of cancer selected from the group consisting of breast cancer, renal cancer, brain tumor, esophageal cancer, leukemia, lymphoma, melanoma, squamous cell carcinoma of the head, neck, uterus or esophagus, adenocarcinoma of the uterus, malignant mixed tumor, hepatocellular carcinoma, basal cell carcinoma, acanthoma-like gingival tumor, tumor of the oral cavity, perianal adenocarcinoma, anal sac tumor, anal sac apocrine adenocarcinoma, sertoli cell carcinoma, cancer of vaginal vestibule, sebaceous adenocarcinoma, sebaceous epithelioma, sebaceous adenoma, sweat gland carcinoma, intranasal adenocarcinoma, nasal adenocarcinoma, thyroid cancer, bronchial adenocarcinoma, adenocarcinoma, ductal carcinoma, breast adenocarcinoma, composite type breast adenocarcinoma, malignant mammary mixed tumor, intraductal papillary adenocarcinoma, fibrosarcoma, hemangiopericytoma, osteosarcoma, chondrosarcoma, soft tissue sarcoma, histiocytic sarcoma, myxosarcoma, undifferentiated sarcoma, mastocytoma, cutaneous leiomyoma, intraperitoneal leiomyoma, leiomyoma, chronic lymphocytic leukemia, gastrointestinal lymphoma, digestive lymphoma, small-cell-to-medium-cell lymphoma, adrenomedullary tumor, granulosa cell tumor, and pheochromocytoma.
2. The method according to claim 1, wherein the polypeptide to be measured is a CAPRIN-1 protein having any one of the amino acid sequences shown in the even-numbered SEQ ID NOS: 2-30 or a polypeptide having 85% or more sequence identity with the CAPRIN-1 protein.
3. The method according to claim 1 or 2, wherein the living organism is a human, a dog, or a cat.
4. The method according to claim 3, wherein the living organism is a dog and the polypeptide to be measured has an amino acid sequence shown in any one of the even-numbered SEQ ID NOS: 2-30.
5. The method according to claim 4, wherein the living organism is a dog and the polypeptide to be measured has the amino acid sequence shown in SEQ ID NO: 6, 8, 10, 12, or 14.
6. The method according to claim 3, wherein the living organism is a human and the polypeptide to be measured has the amino acid sequence shown in SEQ ID NO: 2 or 4.

7. The method according to any one claims 1 to 6, wherein the sample is serum, blood plasma, ascite, or pleural effusion.
8. The method according to any one of claims 1 to 7, wherein the expression of the polypeptide is measured by measuring mRNA encoding the polypeptide, which is contained in the sample.
9. The method according to claim 8, comprising examining the existing amount of the mRNA in the sample using a polynucleotide that specifically hybridizes to a partial sequence of 15 or more nucleotides in the nucleotide sequence of the mRNA.
10. The method according to claim 9, wherein the living organism is a dog and the polynucleotide is a polynucleotide specifically hybridizing to a partial sequence of 15 or more nucleotides in the nucleotide sequence shown in SEQ ID NO: 5, 7, 9, 11, or 13.
11. The method according to claim 10, wherein the living organism is a human and the polynucleotide is a polynucleotide specifically hybridizing to a partial sequence of 15 or more nucleotides in the nucleotide sequence shown in SEQ ID NO: 1 or 3.
12. The method according to any one of claims 1 to 11, comprising further detecting the malignancy of a cancer based on the fact that the malignancy of cancer is high when the expression level of the polypeptide is higher than that of a control.
13. The method according to any one of claims 1 to 12, comprising further detecting the progression of cancer on the basis of the indicator that the extent of cancer is advanced when the expression level of the polypeptide is higher than that of a control.

Fig. 1



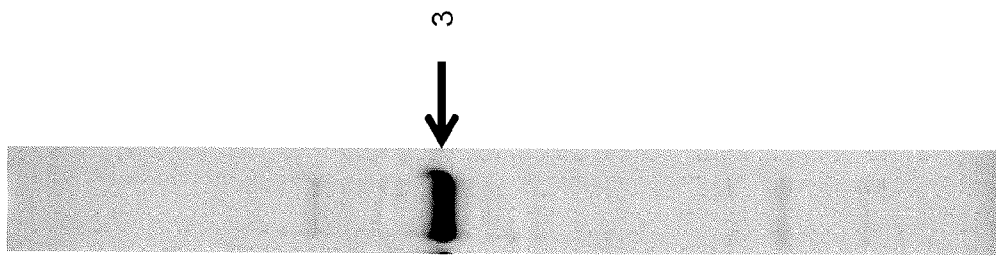


Fig. 2

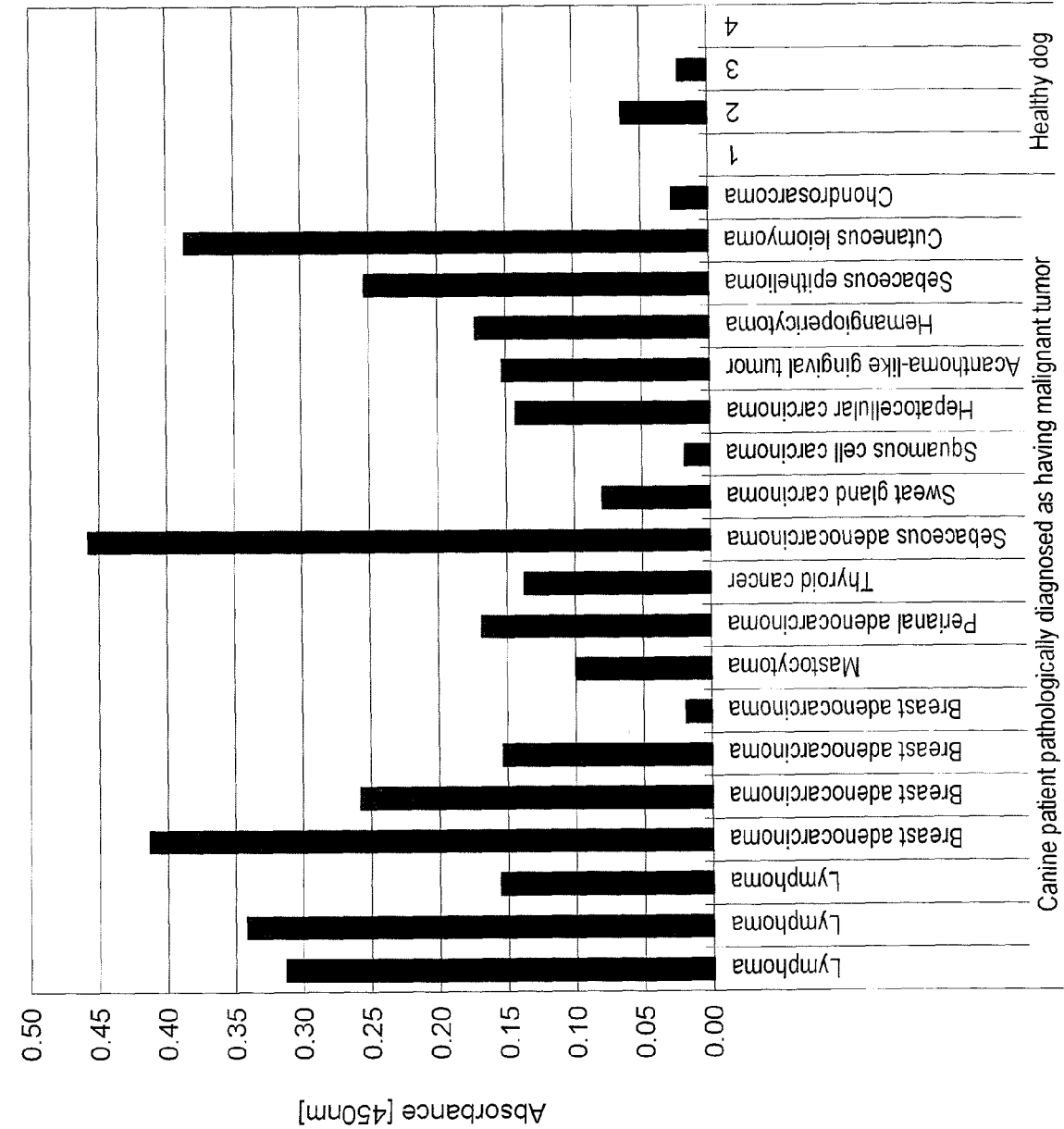
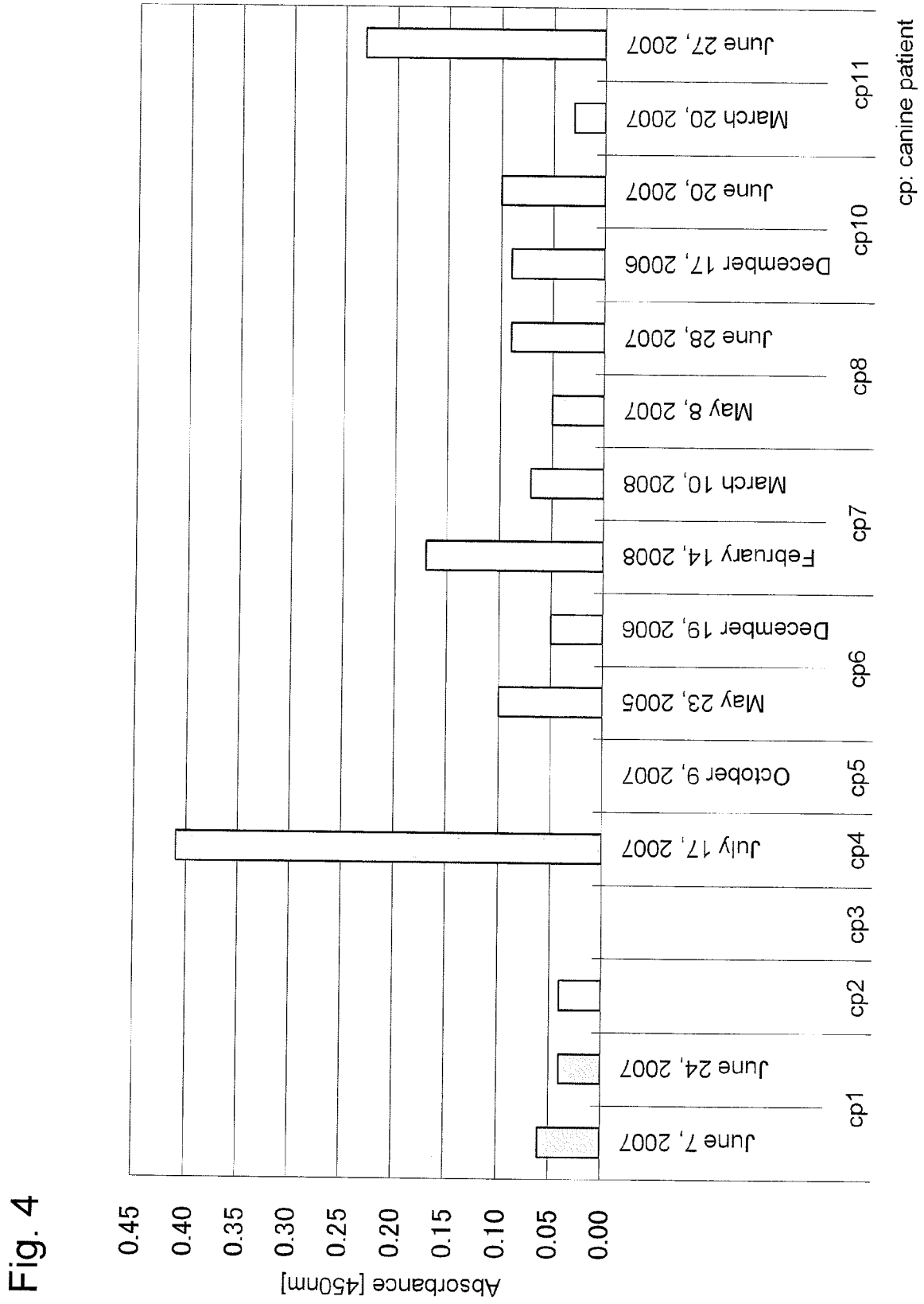


Fig. 3





EUROPEAN SEARCH REPORT

Application Number
EP 14 15 3299

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (IPC)
X	WO 2004/076682 A2 (SURROMED INC [US]) 10 September 2004 (2004-09-10) * claim 17; sequence 54 *	1-13	INV. G01N33/574 C12N15/09 C12Q1/68 G01N33/53
X	US 2008/107668 A1 (PHILIP RAMILA [US] ET AL) 8 May 2008 (2008-05-08) * pages 16,19; claim 44; sequences 50,168 *	1-13	
X	US 2003/190640 A1 (FARIS MARY [US] ET AL) 9 October 2003 (2003-10-09) * page 22; claims 6-7; sequence 354 *	1-13	
X	US 2003/118599 A1 (ALGATE PAUL A [US] ET AL) 26 June 2003 (2003-06-26) * pages 54-55; claim 6; sequences 601-602,666 *	1-13	
X	WO 2004/097051 A2 (WYETH CORP [US]; BURCZYNSKI MICHAEL E [US]; DORNER ANDREW [US]; TWINE) 11 November 2004 (2004-11-11) * pages 56-57 *	1-13	
X	US 2007/154931 A1 (RADICH JERALD P [US] ET AL) 5 July 2007 (2007-07-05) * pages 162,226; claim 1; table 8; sequences 2929,6897 *	1-13	
X	US 2006/019256 A1 (CLARKE MICHAEL F [US] ET AL) 26 January 2006 (2006-01-26) * paragraph [0113]; table 4 *	1-13	
X	US 2006/069054 A1 (HOUGHTON RAYMOND L [US] ET AL) 30 March 2006 (2006-03-30) * paragraphs [0007] - [0008], [0039] - [0042], [0306]; sequence 273 *	1-13	G01N C12Q
		-/--	
The present search report has been drawn up for all claims			
Place of search The Hague		Date of completion of the search 8 April 2014	Examiner Lunter, Pim
CATEGORY OF CITED DOCUMENTS X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document			

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Application Number
EP 14 15 3299

DOCUMENTS CONSIDERED TO BE RELEVANT				
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (IPC)	
X	WO 02/092001 A2 (CORIXA CORP [US]; LODES MICHAEL J [US]; WANG TONGTONG [US]; FAN LIQUN) 21 November 2002 (2002-11-21) * pages 118-119; example 11; sequence 601 *	1-13		
X	WO 2008/031041 A2 (H LEE MOFFITT CANCER CT AND RE [US]; UNIV SOUTH FLORIDA [US]; RIKER AD) 13 March 2008 (2008-03-13) * page 41; table b *	1-13		
X	WO 2006/002378 A2 (AVALON PHARMACEUTICALS [US]; STROVEL JEFFREY W [US]; CAIN COLYN B [US]) 5 January 2006 (2006-01-05) * pages 3, 152; table 1 *	1-13		
X	US 6 335 170 B1 (ORNTOFT TORBEN F [DK]) 1 January 2002 (2002-01-01) * page 394; table 8 *	1-13		
X	WO 2005/007830 A2 (MAYO FOUNDATION [US]; VANAJA DONKENA K [US]; YOUNG CHARLES Y F [US]) 27 January 2005 (2005-01-27) * page 73; table 2 *	1-13		TECHNICAL FIELDS SEARCHED (IPC)
X	US 2004/029114 A1 (MACK DAVID H [US] ET AL) 12 February 2004 (2004-02-12) * page 51; table 4 *	1-13		
X	WO 01/72295 A2 (CORIXA CORP [US]; REED STEVEN G [US]; LODES MICHAEL J [US]; MOHAMATH R) 4 October 2001 (2001-10-04) * L86S-6 *; example 3; sequences 84,93	1-13		
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Place of search The Hague		Date of completion of the search 8 April 2014	Examiner Lunter, Pim	
CATEGORY OF CITED DOCUMENTS X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document				

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**ANNEX TO THE EUROPEAN SEARCH REPORT
ON EUROPEAN PATENT APPLICATION NO.**

EP 14 15 3299

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08-04-2014

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2004076682 A2	10-09-2004	NONE	
US 2008107668 A1	08-05-2008	AU 2007343683 A1 CA 2661651 A1 EP 2061503 A2 US 2008107668 A1 WO 2008088583 A2	24-07-2008 24-07-2008 27-05-2009 08-05-2008 24-07-2008
US 2003190640 A1	09-10-2003	NONE	
US 2003118599 A1	26-06-2003	NONE	
WO 2004097051 A2	11-11-2004	AU 2004235382 A1 CA 2524173 A1 EP 1629119 A2 US 2005202451 A1 US 2007198198 A1 WO 2004097051 A2	11-11-2004 11-11-2004 01-03-2006 15-09-2005 23-08-2007 11-11-2004
US 2007154931 A1	05-07-2007	US 2007154931 A1 US 2012072124 A1	05-07-2007 22-03-2012
US 2006019256 A1	26-01-2006	AU 2004256425 A1 AU 2008202471 A1 CA 2528669 A1 EP 1639090 A2 EP 2003196 A2 EP 2481814 A2 JP 2007516693 A KR 20060031809 A US 2006019256 A1 US 2008292546 A1 US 2012315216 A1 US 2013244256 A1 WO 2005005601 A2	20-01-2005 26-06-2008 20-01-2005 29-03-2006 17-12-2008 01-08-2012 28-06-2007 13-04-2006 26-01-2006 27-11-2008 13-12-2012 19-09-2013 20-01-2005
US 2006069054 A1	30-03-2006	US 2003166022 A1 US 2006069054 A1 US 2008200386 A1 US 2008206250 A1 US 2008207486 A1 US 2008207511 A1 US 2008207547 A1 US 2008207548 A1 US 2008227739 A1 US 2011104211 A1	04-09-2003 30-03-2006 21-08-2008 28-08-2008 28-08-2008 28-08-2008 28-08-2008 28-08-2008 18-09-2008 05-05-2011

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**ANNEX TO THE EUROPEAN SEARCH REPORT
ON EUROPEAN PATENT APPLICATION NO.**

EP 14 15 3299

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report.
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08-04-2014

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 02092001 A2	21-11-2002	AU 2002311909 A1 EP 1516049 A2 WO 02092001 A2	25-11-2002 23-03-2005 21-11-2002
WO 2008031041 A2	13-03-2008	US 2008113360 A1 WO 2008031041 A2	15-05-2008 13-03-2008
WO 2006002378 A2	05-01-2006	NONE	
US 6335170 B1	01-01-2002	AU 3316600 A US 6335170 B1 US 2004038207 A1 WO 0052204 A2	21-09-2000 01-01-2002 26-02-2004 08-09-2000
WO 2005007830 A2	27-01-2005	US 2007048738 A1 WO 2005007830 A2	01-03-2007 27-01-2005
US 2004029114 A1	12-02-2004	NONE	
WO 0172295 A2	04-10-2001	AU 6100701 A CA 2404233 A1 CZ 20023567 A3 HU 0500345 A2 JP 2004526401 A PL 366626 A1 WO 0172295 A2	08-10-2001 04-10-2001 12-11-2003 28-07-2005 02-09-2004 07-02-2005 04-10-2001

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REFERENCES CITED IN THE DESCRIPTION

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Patent documents cited in the description

- US 20080075722 A [0017]
- WO 2005100998 A [0017]
- JP 2008202320 A [0146]

Non-patent literature cited in the description

- *J Biol Chem.*, 1995, vol. 270, 20717-20723 [0016] [0017]
- *J Immunol.*, 2004, vol. 172, 2389-2400 [0016] [0017]
- **KARLIN ; ALTSCHUL.** *Proc. Natl. Acad. Sci. U.S.A.*, 1993, vol. 87, 2264-2268 [0035]
- **ALTSCHUL et al.** *Nucleic Acids Res.*, 1997, vol. 25, 3389-3402 [0035]
- Molecular Cloning. **SAMBROOK ; AUSUBEL et al.** *Current Protocols in Molecular Biology.* Cold Spring Harbor Laboratory Press [0038]
- *Short Protocols in Molecular Biology. A Compendium of Methods from Current Protocols in Molecular Biology*, 1995 [0038]

专利名称(译)	癌症检测方法		
公开(公告)号	EP2733492A1	公开(公告)日	2014-05-21
申请号	EP2014153299	申请日	2009-08-05
[标]申请(专利权)人(译)	东丽株式会社		
申请(专利权)人(译)	TORAY INDUSTRIES , INC.		
当前申请(专利权)人(译)	TORAY INDUSTRIES , INC.		
[标]发明人	OKANO FUMIYOSHI SUZUKI KANA		
发明人	OKANO, FUMIYOSHI SUZUKI, KANA		
IPC分类号	G01N33/574 C12N15/09 C12Q1/68 G01N33/53		
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优先权	2008202320 2008-08-05 JP		
其他公开文献	EP2733492B1		
外部链接	Espacenet		

摘要(译)

本发明涉及一种检测癌症的方法，包括测量具有与抗CAPRIN-1蛋白抗体结合的反应性的多肽的表达，所述CAPRIN-1蛋白具有偶数编号的SEQ ID NOS中任一所示的氨基酸序列：序列表中的2-30通过与生物体分离的样品中的抗原 - 抗体反应，以及用于检测包含CAPRIN-1蛋白或其片段的癌症的试剂，针对CAPRIN-1蛋白的抗体或其片段，或编码CAPRIN-1蛋白质或其片段的多核苷酸。

